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STIC-Biotech/ChemLib

9

From: Sent:

Chan, Christina

Wednesday, November 12, 2003 1:00 PM Walicka, Malgorzata

To: Cc: STIC-Biotech/ChemLib

Subject:

RE:

Please rush. Thanks Chris

Chris Chan TC 1600 New Hire Training Coordinator and SPE 1644 308-3973 CM-1, 9B19

----Original Message----

From:

Walicka, Malgorzata

Sent:

Tuesday, November 11, 2003 1:40 PM

T :

Chan, Christina

Cc:

STIC-Biotech/ChemLib

Subject:

Please search the polypeptide of SEQ ID NO:

112,

113,

114,

115,

116, and 117

in application No. 09/843,676. Please use the CFR of 08/854,050. Please, RUSH.

Thank you in advance.

Malgorzata A. Walicka, Ph.D. Patent Examiner Recombinant Enzymes-Art Unit 1652 **USPTO** 1911 S. Clark Street, Crystal Mall 1, Room 10D06 Mail Room 10D01 Arlington, VA 22202 (703) 305-7270 malgorzata.walicka@uspto.gov

| Searcner: | |
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| Phone: | |
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| Patent Family:_ | |
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Searched:

Database

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Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis;
prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
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AAY26580
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96US-0724643.
97US-0846017.
97US-0851843.
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97US-091312.
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(GERO-) GERON CORP
Homo sapiens
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18-APR-1997;
25-APR-1997;
06-MAY-1997;
09-MAY-1997;
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        GenCore version 5.1.6
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                                                                                                                                                                                                                                                                          1107863 seqs, 158726573 residues
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Score

Result

1114 1114 1107 1107 1107 1107

Lingner J;

Harley C,

(UYTE-) UNIV TECHNOLOGY CORP.

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The present sequence represents an antigenic peptide from human telomerase reverse transcriptase (hrRT), from the present invention. The present invention also describes the following methods: (A) determining present invention also describes the following methods: (A) determining the change whether a test compound is a modulator of hrRT, by detecting the change compound; (B) preparation of polymucleotide, on administration of the compound; (C) protein preparation of the hrRT with a telomerase BNA component; (C) protein preparation of hrRT with a telomerase RNA component; (C) protein of the hrRT RNA or protein in a sample by binding a relevant certain of the hrRT RNA or protein in a sample by binding a relevant certain of the hrRT RNA or protein of and detecting the product and correlating the presence of probe or amplification product with presence of hrRT in the sample; (C) hrRT expression; and (E) the use of an agent that causes an increase in complex or amplification of hrRT and the polymucleotide encoding ageing. A protein preparation of hrRT and the polymucleotide encoding consecution to age of an agent that inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be effect of ageing or cancer. Inhibitors of telomerase activity can be considered by a protein preparation of hrRT can also be used in the manufacture of medicaments for inhibiting the consecution of hrRT can also be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be consecuted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein;
                                                                                                     Pure and recombinant human Telomerase Reverse Transcriptase and variants - are useful in the diagnosis, prognosis and treatment cell proliferation conditions especially cancer and ageing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human telomerase reverse transcriptase antigenic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 114; DB 19;
Best Local Similarity 100.0%; Pred. No. 3.4e-11;
Matches 23; Conservative 0; Mismarches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ROHLKRVOLRDVSEAEVROHREA 23
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                        Chapman KB,
Harley CB;
                                                                                                                                                                                        Example 8; Fig 54; 387pp; English.
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                            Andrews WH, Cech TR,
Morin GB, Nakamura T,
                                                                                  WPI; 1998-171633/16
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25-KPR-1997;
06-MAY-1997;
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The present sequence represents an antigenic peptide from human closures reverse transcriptes (hTRT), from the present invention. The telomerase reverse transcriptes (hTRT), from the present invention. The present invention also describes the following methods: (A) determining present invention also describes the following methods: (A) determining compound is a modulator of hTRT, by detection of the compound is a modulator of hTRT, by detecting a compound; (B) preparation of recombinant telomerase by contacting a compound; (B) preparation of hTRT with a telomerase by contacting a relevant correlation of the hTRT RNA or protein in a sample by binding a relevant complex to the sample and detecting the complex formed or in the case of probe to the sample and detecting the protein of a vertebrate cell by increasing and (D) increasing the proliferation of a vertebrate cell by increase in complex or amplification product with presence of hTRT in the sample cell vertebrate cell proliferation of an agent that causes an increase in threat on the proliferation of hTRT and the polymucleotide encoding ageing. A protein preparation of hTRT and the polymucleotide encoding confert of againg or cancer. Inhibitors of telomerase activity can be effect of againg or cancer. Inhibitors of telomerase activity and the new activity. A protein preparation of hTRT can also be used in the new activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                           Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing
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                                                                                                         Lingner J;
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100.0%; Pred. No. 3.4e-11;
tive 0; Mismatches 0;
                                                                                                            Harley C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of the specification.
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Harley CB;
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                                                                           (UYTE-) UNIV TECHNOLOGY CORP.
97US-0854050.
97US-0911312.
97US-0912951.
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Morin GB, Nakamura T,
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                                                                                                                                                              WPI; 1998-171633/16.
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23;

Length Indels

WPI; 1999-208111/18

N-PSDB; AAX15924

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The present invention relates to a polypeptide comprising a 20 amino acid sequence derived from human telomerase catalytic subunit (or human telomerase reverse transcriptase, hTERT) amino acid residues 537-556, or fragments thereof comprising at least 10 amino acids and at least two human leukocyte antigen (HLA) class I or class II epitopes. The invention also describes a polypeptide having the above 20 amino acid peptide sequence as additional C- and/or N-terminal sequences on a fragment of hTERT which is not more than 100 amino
                                                                  New catalytic protein of telomerase of a higher animal and a gene coding it - useful for diagnosis of diseases caused by the change in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; telomerase catalytic subunit; hTERT; human leukocyte antigen; human telomerase reverse transcriptase; HLA epitope; cancer; HLA profile; breast cancer; pancreatic cancer; colorectal cancer; lung cancer; ovarian cancer; carcincal cancer; malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma; anti-cancer; mutant; cytostatic; HLA class I epitope; HLA class II epitope; mutein.
                                                                                                                                                                      The specification describes a human catalytic telomerase protein. The products are useful in drug compositions for the diagnosis of diseases caused by the change in activity of telomerase. The present sequence appears in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hTERT fragment with HLA containing polypeptide at its N-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide with an additional C-terminal and/or N-terminal sequence, useful for preparing anti-cancer vaccines
                                                                                                                                                                                                                                                                                            100.0%; Score 114; DB 20;
100.0%; Pred. No. 2.7e-10;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moller M;
                                                                                                                                                                                                                                                                                                                                                                1 ROHLKRVOLRDVSEAEVROHREA 23
                                                                                                                                                                                                                                                                                                                                                                                    49 RQHLKRVQLRDVSEAEVRQHREA 71
                                                                                                                                      Example 1; Page 14; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG71627 standard; protein; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 1; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-FEB-2002; 2002WO-NO00069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-2001; 2001GB-0005238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eriksen JA, Gaudernack G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 23; Conservative
                                                                                       coding it - useful for di
activity of a telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-750459/81.
                                                                                                                                                                                                                                                            131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GEMV-) GEMVAX AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200270679-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG71627;
                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                            Query Match
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Length 131; Indels

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acids of hTERT. The polypeptides of the invention are useful in a pharmaceutical composition or in a vaccine for preventing or treating cancer in populations of individuals having varying HLA profiles. The polypeptides are also useful in a diagnostic kit for diagnosing cancers such as breast, pancreatic, colorectal, lung, ovarian or cervical cancer, malignant melanoma, leukaemia, lymphoma or biliary tract carcinoma. The polypeptides or encoding polymolectide sequences are useful for performing identity, sequence homology and/or hybridisation studies, for predicting structure and/or function (e.g. anti-cancer activity), or for screening methods in drug development or drug screening procedures. The present sequence represents a hTERT fragment with the 20 amino acid HLA epitope containing polypeptide at its N-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human telomerase reverse transcriptase protein from cDNA clone 712562.
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pure and recombinant human Telomerase Reverse Transcriptase and variants - are useful in the diagnosis, prognosis and treatment cell proliferation conditions especially cancer and ageing
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                                                                                                                                                                                                                                                        Length 100;
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lingner J;
                                                                                                                                                                                                                                                     93.9%; Score 107; DB 23; 91.3%; Pred. No. 2.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harley C,
                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                   54 RQHLKRVQLRELSEAEVRQHREA 76
                                                                                                                                                                                                                                                                                                                1 ROHLKRVOLRDVSEAEVROHREA 23
                                                                                                                                                                                                                                                                                                                                                                                                                       AAW46998 standard; Protein; 259 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chapman KB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 19; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GERO-) GERON CORP.
(UYTE-) UNIV TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                  91.3%;
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96US-0724643.
97US-0844419.
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97US-0851843.
97US-0854050.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                  Local Similarity 91.3
les 21; Conservative

    Gech TR, Control Nakamura T,

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                                                                                                                                                                                                                      100 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-APR-1998
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01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-APR-1997
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                                                                                                                                                                                                                      Sequence
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Matches
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Mismatches

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21; Conservative

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cc recombinant protein or polynucleotide, on administration of the compound; recombinant protein or polynucleotide, on administration of the compound; cc (B) preparation of recombinant telemerase by contacting a protein of recombinant telemerase by contacting a protein of preparation of recombinant telemerase by contacting a presention of preparation of hTRT with a telemerase RNA component; (C) detection of the hTRT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, camplifying the product and correlating the presence of hTRT in the sample; and (D) amplification product with presence of hTRT in the sample; and (D) amplification product with presence of hTRT in the sample; and (B) the use of an agent that causes an increasing hTRT increasing the proliferation of a vertebrate cell by increasing hTRT can be used in the manufacture of medicaments for inhibiting the MTRT and the polynucleotide encoding cellect of ageing or cancer. Inhibitors of telomerase activity can be effect to ageing a protein preparation of hTRT can also be used in the new conditions that are associated with high telomerase activity. A protein preparation of hTRT can also be used in the new conditions that are associated with high telomerases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the human telomerase reverse transcriptase thing the furgraph invention relates to a monoclonal antibody recognising the hrbra. The antibody can be used for the investigation, diagnosis and treatment of telomerase-related diseases, especially diseases in which telomerase expression is up-regulated e.g. cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New monoclonal antibody recognizing human telomerase catalytic subunit (hTERT) useful for treating and diagnosing cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anazawa H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human telomerase reverse transcriptase; hTERT; antibody; diagnosis;
telomerase-related disease; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                        ch 93.9%; Score 107; DB 19; Length 259; 1 Similarity 91.3%; Pred. No. 7.8e-09; 21; Conservative 2; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Furuya A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human telomerase reverse transcriptase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 72-73; 78pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ROHLKRVOLRDVSEAEVROHREA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY43128 standard; Protein; 283 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shibata
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91.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-591316/50.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                              259 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9950407-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42
                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                               methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
AAY43128
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel gene, useful in detection of telomerase activity and cancer cells as well as screening telomerase inhibitors for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                    CRT-1; reverse transcriptase; telomerase; inhibitor; detection; telomerase activity; cancer cell; screening; human.
                                                                                                                                                                                                                                        /note= "Partial sequence, no stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ROHLKRVOLRDVSEAEVROHREA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY25462 standard; Protein; 438 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 31-32; 44pp; Japanese.
                                                                                                                                                                                                                Location/Qualifiers
           23
                                                                         AAY25461 standard; Protein; 437 AA.
1 ROHLKRVOLRDVSEAEVROHREA
                                                                                                                                                                                                                            1..437
/label= CRT-1
                                                                                                                                                                                                                                                                                                                                               98JP-0013232.
98JP-0033584.
                                                                                                                                                                                                                                                                                                                                    98JP-0139177.
                                                                                                                                                                                                                                                                                                                 99WO-JP00039
                                                                                                                                                                                                                                                                                                                                                                               (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     Yoshida K;
                                                                                                                                          Human CRT-1 protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-430393/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  437 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAX88243
                                                                                                                                                                                                                                                                                                                                          06-MAY-1998;
08-JAN-1998;
30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                       rsuchiya M,
                                                                                                                                                                                                                                                                                                                     08-JAN-1999;
                                                                                                                                                                                                                                                                            WO9935261-A1
                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                        22-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancers
                                                                                                   AAY25461;
                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
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                                                            RESULT 7
                                                                        AAY25461
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/note= "glutathione-S-transferase fragment"

1..221

Region Region

249..531 /note= "hTRT protein fragment"

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                        Novel gene, useful in detection of telomerase activity and cancer cells as well as screening telomerase inhibitors for treatment of
                                                             CRT-1; reverse transcriptase; telomerase; inhibitor; detection; telomerase activity; cancer cell; screening; human.
                                                                                                                                                               /note= "Partial sequence, no stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 107; DB 20; Length 438;
Pred. No. 1.5e-08;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 35-36; 44pp; Japanese.
                                                                                                                               Location/Qualifiers
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                                                                                                                                         1..438
/label= CRT-1
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98JP-0013232.
98JP-0033584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 91.3%;
Matches 21; Conservative
                                                                                                                                                                                                                                           99WO-JP00039
                                                                                                                                                                                                                                                                                                                  CHUS ) CHUGAI SEIYAKU KK.
                                     Human CRT-1 protein #2
                                                                                                                                                                                                                                                                                                                                            fsuchiya M, Yoshida K;
                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-430393/36.
N-PSDB; AAX88250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         438 AA;
                                                                                                                                                                                                                                                               06-MAY-1998;
08-JAN-1998;
30-JAN-1998;
                                                                                                    Homo sapiens
                                                                                                                                                                                       WO9935261-A1
                                                                                                                                                                                                                                         08-JAN-1999;
              22-SEP-1999
                                                                                                                                                                                                                15-JUL-1999
                                                                                                                           Key
Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                    cancers
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Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing

Example 6; Page 225; 387pp; English

Lingner J;

Harley C,

Chapman KB, Harley CB;

Andrews WH, Cech TR, Morin GB, Nakamura T,

WPI; 1998-171633/16.

(UYTE-) UNIV TECHNOLOGY CORP.

GERON CORP.

(GERO-)

14-AUG-1997;

960S-0724643. 970S-0844419. 970S-0846017. 970S-0851843. 970S-0854050. 970S-0911312.

06-MAY-1997 09-MAY-1997

97GB-0020890 97US-0915503

01-OCT-1997;

14-AUG-1997

18-APR-1997 25-APR-1997

GB2317891-A. 08-APR-1998

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The present sequence represents a fusion protein from an example of the present invention which describes human telomerase reverse transcriptes (hTRT). The present invention also describes the fullowing methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein preparation of hTRT with a telomerase by contacting a protein of the hTRT with a telomerase by contacting a protein probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of hTRT in the sample; and (D) increasing the product with presence of hTRT in the sample; and (D) increasing the product with presence of hTRT in the sample; and (D) increasing the product with presence of hTRT in the sample; and (D) increasing the product with presence of hTRT in the sample; and (D) increasing the product with presence of hTRT in the sample; and (D) increasing the product with presence of hTRT in the sample; and (D) increasing the product with a vertebrate cell by increasing hTRT expression; and (E) the use of an agent that causes an increase in the manufacture of medicament that inhibits desired to again or cancer. Inhibitors of telomerase activity can be used in the manufacture of endicaments for inhibiting the read to the transfer of adelinerase activity can be used in the manufacture of endicaments for inhibiting the read to the product with the produ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used to treat conditions that are associated with high telomerase activity. A protein preparation of hTRT can also be used in the new
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290 RQHLKRVQLRELSEAEVRQHREA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROHLKRVOLRDVSEAEVROHREA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW56109 standard; Protein; 564 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           531 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW56109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW56109
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80 RQHLKRVQLRELSEAEVRQHREA 102

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AAW47002 standard; Protein; 531 AA.

RESULT 9 AAW47002

Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.

Location/Qualifiers

Homo sapiens

Key

Synthetic

Glutathione-S-transferase and hTRT fusion protein 2.

13-AUG-1998 (first entry)

AAW47002;

42 RQHLKRVQLRELSEAEVRQHREA 64

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93.9%; Score 107; DB 19; Length 564; 91.3%; Pred. No. 2e-08; cive 2; Mismatches 0; Indels C
                                                                                                                  (UYTE-) UNIV TECHNOLOGY CORP.
                                                                                                                            Andrews WH, Cech TR,
Morin GB, Nakamura T,
                                                                                                                                                                                                                                                                564 AA;
                                                                                                                                        1998-171633/16.
                                                                                                                 CORP.
                                                                                                                                            N-PSDB; AAV22426.
                                                                                                                 GERO-) GERON
                                                                                                                                                                                                                                                                Sequence
                                                                                                         14-AUG-1997;
                                                                      01-OCT-1997;
                                                                              14-AUG-1997;
01-OCT-1996;
                               Homo sapiens
                                                                                                  09-MAY-1997
                                                                                                      14-AUG-1997
                                                                                     18-APR-1997
                                                                                          25-APR-1997
                                                                                              06-MAY-1997
                                                      GB2317891-A
                                                              08-APR-1998
                           Synthetic
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AAW97384;
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                            RESULT 11
                                                    AAW97384
                                                                                                                      원
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a human telomerase reverse transcriptase (hTRT) clone protein from the present invention. The present invention also clone protein from the present invention. The present invention also clone protein following methods: (A) determining whether a test compound (E) a modulator of hTRT, by detecting the change in hTRT recombinant protein or polymucleotide, on administration of the compound; (B) protein or polymucleotide, on administration of the compound; (C) detection of preparation of hTRT with a telomerase RNA component; (C) detection of hTRT with a telomerase RNA component; (C) detection of hTRT with a sample by binding a relevant probe to the cample and detecting the complex formed or in the case of RNA detection, camplifying the product and correlating the presence of complex or camplification product with presence of hTRT in the sample; and (D) amplification product with presence of hTRT in the sample; and (E) the use of an agent that causes an increasing hTRT increasing the proliferation of a vertebrate cell by increasing the cyertebrate cell proliferation of hTRT and the polymucleotide encoding vertebrate cell proliferation of hTRT and the polymucleotide encoding celfect of ageing or cancer. Inhibitors of telomerase activity can be effect of ageing or cancer. Inhibitors of telomerase activity, A protein preparation of hTRT can also be used in the new that are associated with high telomerase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing
                     Human telomerase reverse transcriptase 63 kDa clone 712562 protein.
                                                               Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis;
prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lingner J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chapman KB, Harley C,
Harley CB;
                                                                                                                                                                                                                                                             Misc-difference 102
/label= encoded by ARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 68; 387pp; English.
                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0915503.
96US-0724643.
97US-0844419.
97US-0851843.
97US-0851843.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0911312
97US-0912951
                                                                                                                                                                                                                                                                                                                                                                                                                97GB-0020890
13-AUG-1998 (first entry)
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Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia; neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma; smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour; stem cell differentiation; organ differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                               New catalytic protein of telomerase of a higher animal and a gene coding it - useful for diagnosis of diseases caused by the change in activity of a telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a catalytic telomerase protein. The products are useful in drug compositions for the diagnosis of diseases caused by the change in activity of telomerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 93.9%; Score 107; DB 20; Length 591; Best Local Similarity 91.3%; Pred. No. 2.1e-08; Matches 2; Mismatches 0; Indels Matches 21; Conservative 2; Mismatches 0; Indels
                                                                                                               Catalytic telomerase; diagnosis; disease; telomerase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-terminal truncated telomerase protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ROHLKRVOLRDVSEAEVROHREA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 11-14; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY00636 standard; Protein; 617 AA.
AAW97384 standard; Protein; 591
                                                                                             A catalytic telomerase protein.
                                                                                                                                                                                                                                                                                                                    (MITU ) MITSUBISHI CHEM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                     97JP-0207708.
                                                                                                                                                                                                                                                       97JP-0207708
                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-208111/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                591 AA;
                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAX15923
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Synthetic.
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                                                                                                                                                                                                                                                            01-AUG-1997;
                                                                                                                                                                                                                                                                                           01-AUG-1997;
                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                               JP11046768-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY00636;
                                                                                                                                                                                                                                23-FEB-1999.
                                                                      14-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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21; Conservative

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Gaps

98WO-US13835

01-JUL-1998;

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This invention describes novel human CRT-1 genes and their encoded proteins containing a reverse transcriptase motif, which act as telomerase inhibitors. The gene, its encoded protein and derived antibodies can be used to provide base sequence information, detect telomerase activity and cancer cells, and to screen telomerase inhibitors. The detection method is simple and effective.
                                                                                                                                                                                                                Novel gene, useful in detection of telomerase activity and cancer cells as well as screening telomerase inhibitors for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lingner J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human telomerase reverse transcriptase Delta182 variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.9%; Score 107; DB 20;
91.3%; Pred. No. 2.2e-08;
iive 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harley C,
                                                                                                                                                                                                                                                                                   Example 1; Page 37-39; 44pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ROHLKRVQLRDVSEAEVROHREA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW46997 standard; Protein; 807 AA.
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Harley CB;
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970S-0844419.
970S-0846017.
970S-0851843.
970S-0911312.
970S-0912951.
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                                 98JP-0139177.
 99WO-JP00039
                                                                  98JP-0033584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97GB-0020890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0915503
                                                                                                 (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Conservative
                                                                                                                                ľsuchiya M, Yoshida K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andrews WH, Cech TR, Morin GB, Nakamura T,
                                                                                                                                                                 WPI; 1999-430393/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GERON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                        622 AA;
                                                                                                                                                                                   N-PSDB; AAX88251
 08-JAN-1999;
                               06-MAY-1998;
                                                  08-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GB2317891-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAY-1997
09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW46997;
                                                                                                                                                                                                                                                  cancers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW46997
ID AAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is a truncated human telomerase of the invention. Primers that amplify the telomerase coding sequence can be used in a method for diagnosing cancer in a patient. The telomerase can be used for detection, diagnosis and drug screening. Inhibitors of telomerase activity can be used to treat cancers such as melanomas, other skin cancers, neuroblastomas, breast carcinomas, colon carcinomas, colon skin growths. Enhancers of telomerase may be used to stimulate stem cell proliferation and differentiation (expansion of haematopoietic stem cells could be administered in the bone marrow transplant context). As well, many tissues have stem cells. Proliferation of these cells may be useful in wound healing, hair growth, treatment of disease such as wilm's tumour, organ regeneration or differentiation after injury or house. The Crterminus of this sequence can be replaced by the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                     New isolated vertebrate telomerase genes - used to develop products for treating cancers or for organ regeneration, nerve cell or brain cell growth following injury or bone marrow transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRT-1; reverse transcriptase; telomerase; inhibitor; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Partial sequence, no stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 93.9%; Score 107; DB 20; Length 617; l Similarity 91.3%; Pred. No. 2.2e-08; 21; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    telomerase activity; cancer cell; screening; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ROHLKRVQLRDVSEAEVROHREA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                        Claim 4; Fig 11b-c; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY25463 standard; Protein; 622 AA.
                                                                                                                        (CAMB-) CAMBIA BIOSYSTEMS LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= CRT-1
                                      97US-0051410.
                                                                       97US-0053329.
                        97US-0058287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human CRT-1 protein #3
                                                                                                                                                         Bowtell D, Kilian A;
                                                                                                                                                                                      WPI; 1999-106060/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 617 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                        N-PSDB; AAX18264
                                                                                     04-AUG-1997;
                      09-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-SEP-1999
                                      01-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09935261-A1
                                                                         21-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY25463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Best Loca Matches

ò g AAY25463

Protein

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Gaps

Bowtell D, Kilian A; WPI; 1999-106060/09.

N-PSDB; AAX18265

New isolated vertebrate telomerase genes - used to develop products for treating cancers or for organ regeneration, nerve cell or brain cell growth following injury or bone marrow transplantation

Claim 4; Fig 11d-e; 134pp; English.

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WPI; 1998-171633/16.
 N-PSDB; AAV22382
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The present sequence represents a human telomerase reverse transcriptase (hRRT) variant from the present invention. The present invention also cascribes the following methods: (A) determining whether a test compound ce describes the following methods: (A) determining whether a test compound compound to a modulator of hTRT, by detecting the change in hTRT recombinant protein or polyuncleofide, on administration of thTRT recombinant telomerase by contacting a protein of preparation of hTRT with a telomerase RNA component; (C) detection of preparation of hTRT with a telomerase RNA component; (C) detection of hTRT RNA or protein in a sample by binding a relevant probe to the the hTRT RNA or protein in a sample by binding a relevant probe to the camplifying the product and correlating the presence of complex or amplifying the proliferation of a vertebrate cell by increasing hTRT camplifying the proliferation of an agent that causes an increase in cell expression; and (E) the use of an agent that causes an increase in cell captures of a geing A protein preparation of create a medicament that inhibits of the modern of a protein preparation of a protein cample of a condition of a create a medicament of the cinition of the manufacture of medicaments for inhibiting the the manufacture of the proliferation of the manufacture of the polymorleoptic province of telomerase activity can be used in the manufacture of the clomerase activity can be used to treat conditions that are associated with high telomerase activity can be necessariant that are associated with high telomerase activity of the proliferation of them and a protein of the proliferation of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity. A protein preparation of hTRT can also be used in the new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                           Pure and recombinant human Telomerase Reverse Transcriptase and variants - are useful in the diagnosis, prognosis and treatment cell proliferation conditions especially cancer and ageing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 93.9%; Score 107; DB 19; Length 807; Best Local Similarity 91.3%; Pred. No. 3e-08; Mismatches 2; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ROHLKRVOLRDVSEAEVROHREA 23
                                                                                                                                                                                                                                                                                                               Disclosure; Fig 20; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 807 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia; neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma; smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour; stem cell differentiation; organ regeneration; organ differentiation.

(CAMB-) CAMBIA BIOSYSTEMS LLC.

04-NUG-1997;

97US-0058287. 97US-0051410. 97US-0053018. 97US-0053329. 97US-0054642.

> 01-JUL-1997 21-JUL-1997 21-JUL-1997

98WO-US13835.

01-JUL-1998; 09-SEP-1997;

WO9901560-A1

14-JAN-1999

Homo sapiens

Synthetic.

N-terminal truncated telomerase protein sequence.

26-JUL-1999 (first entry)

AAY00637;

AAY00637 standard; Protein; 807 AA.

RESULT 15 AAY00637

```
This sequence is a truncated human telomerase of the invention. Primers that amplify the telomerase coding sequence can be used in a method for diagnosing cancer in a patient. The telomerase can used in a method for diagnosing cancer in a patient. The telomerase can be used for detection, diagnosis and drug screening. Inhibitors of telomerase activity can be used to treat cancers such as melanomas, other telomerase activity can be used to treat cancers con carcinomas, colon carcinomas, skin cancers, lymphomas, osteosarcomas or smooth muscle cell hyperplasias col skin growths. Enhancers of telomerase may be used to stimulate stem cell proliferation and differentiation (expansion of haematopoietic stem cells could be administered in the bone marrow transplant context). As cells many tissues have stem cells. Proliferation of these cells may be useful in wound healing, hair growth, treatment of disease such as Wilm's tumour, organ regeneration or differentiation after injury or diseases, there cell or brain cell growth following injury.
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1 Similarity 91.3%; Score 107; DB 20; Length 807;
21; Conservative 2; Mismatches 0; Indels C
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Job time : 28.6415 secs
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Best Local &
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Sequence
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Sequence
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Sequence 113, Application US/08851843A

Patent No. 6093809

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

APPLICANT: Lingner, Joachim

APPLICANT: Chapman, Karen B.

APPLICANT: Chapman, Karen B.

APPLICANT: Andrews, William H.

TITLE OF INVENTION:

APPLICANT: Andrews, William H.

TITLE OF INVENTION:

APPLICANT: Andrews, William H.

TITLE OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United Stare-

ZIP: ALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARES PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION
PRIOR APPLICATION
PRIOR APPLICATION
PRIOR APPLICATION UNMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
CLASSIFICATION:
 US-08-974-549A-2
US-08-974-549A-344
US-08-854-050-225
US-09-430-323-225
US-09-123-334-2
US-09-675-331-2
US-08-974-549A-611
US-08-912-951-323
US-08-912-951-325
US-08-974-549A-612
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US-08-912-951-334
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                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BIR PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REPERENCE/DOCKET NUMBER: 0153
TELECOMMUNICATION INFORMATION:
TELEFONE: (415) 576-0200
IELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 113:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36,429
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 1007
1007
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 Sequence 113, App
Sequence 233, App
Sequence 113, App
Sequence 113, App
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                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                              1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
        5.1.6
Compugen Ltd.
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US-08-974-559A-233
US-08-854-050-113
US-09-430-333-113
US-08-912-951-114
US-08-812-851-114
US-08-854-650-67
US-08-854-050-67
US-08-912-951-13
US-08-912-951-10
US-08-912-951-10
US-08-912-951-10
US-08-912-951-10
US-08-912-951-10
US-08-912-951-10
US-08-912-951-10
US-08-912-951-318
US-08-912-951-318
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S-08-851-843A-101
S-08-974-549A-267
S-08-854-050-101
                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -08-974-549A-5 ·
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                                                                                                                                                                                                      328717 seqs, 42310858 residues
       GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                  114
1 RQHLKRVQLRDVSEAEVRQHREA 23
                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                OM protein - protein search, using sw model
                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                      Issued Patents AA;*
                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                       US-08-854-050-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                    Database
                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPEP: Floppadible

COMPUTER: IBM PC compatible

CURRENT SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PACHILIN Release #1.0, Version #1.30

CURRENT PEPLICATION DATA:

APPLICATION NUMBER: US/08/854,050

FILING DATE: 06-MAY-1997

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/846,017

FILING DATE: 06-MAY-1997

CLASSIFICATION: 536

PRIOR APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

CLASSIFICATION NUMBER: US 08/844,419

PILING DATE: 18-APR-1997

FILING DATE: 18-APR-1997

FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cech, Thomas R.
APPLICANT: Cech, Thomas R.
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
                                               WO PCT/US97/17885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ROHLKRVQLRDVSEAEVROHREA 23
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; Sequence 113, Application US/08854050
; Parent No. 6261836
PILING DATE: 01-OCT-1997
PRIOR APPLICATION DATE: WO PCT/US9
APPLICATION NUMBER: WO PCT/US9
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT: INFORMATION:
NAME: APPLE, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01538
TELECHONE: (415) 576-0200
TELEPAX: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 233:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-233
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                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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                                                                                                                                                                                                                        DB 3; Length 23;
                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Calvin B.
APPLICANT: Hunerey, William H.
APPLICANT: Hunen Telomerase Catalytic Subunit
MINBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94111-3834

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
EDDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION NUMBER: US 08/724,643
APPLICATION NUMBER: US 08/844,419
FILING DATE: 01-OCT-1996
PRIOR APPLICATION NUMBER: US 08/844,419
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-WAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 09-WAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-WAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Bighth Floor
                                                                                                                                                                                                                                  100.0%; Score 114; DB 3
100.0%; Pred. No. 1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO PCT/US97/17618
                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US OR/917
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 233, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                           1 ROHLKRVQLRDVSEAEVROHREA 23
                                                                                                                                                                                                                                                                                                                                                              1 RQHLKRVQLRDVSEAEVRQHREA 23
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 23; Conservative
                                          SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: peptide US-08-851-843A-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-974-549A-233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
```

```
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Cech, Thomas R.
APPLICANT: Chapman, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
TITLE OF INVENTION: THEREBEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 114; DB 4; Length 23; Best Local Similarity 100.0%; Pred. No. 1e-11; Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FLING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

CLASSIFICATION 1435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

CLASSIFICATION:

APPLICATION NUMBER:

CLASSIFICATION:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

CLASSIFICATION NUMBER:

FILING DATE:

FILING DATE:

FILING DATE:

FILING DATE:

FILING DATE:

FILING DATE:

CLASSIFICATION NUMBER:

FILING DATE:

FILING DATE:

CLASSIFICATION:

APPLICATION NUMBER:

RELING DATE:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ASSIFICATION:

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CLASSIFICATION:

ASSIFICATION:

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CLASSIFICATION:

ASSIFICATION:

ASSIFICAT
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                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-09-430-323-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States of America ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ROHLKRVQLRDVSEAEVROHREA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RQHLKRVQLRDVSEAEVRQHREA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 114, Application US/08912951
Patent No. 6475789
                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                     TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
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COMPUTER READABLE FORM:
    WEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/430,323
    FILING DATE: 29-Oct-1999
    CLASSIFCATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-430-323-113

i Sequence 113, Application US/09430323

i Sequence 113, Application US/09430323

i GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 015389-002930US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-MR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ROHLKRVQLRDVSEAEVROHREA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RQHLKRVQLRDVSEAEVRQHREA 23
                                                                                                NAME: Apple, Randolph T.
REGISTRATION UNMBER: 36,429
REFERENCE/DOCKET NUMBER: 01536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAK: (415) 576-0300
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: California
                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS:
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Gaps
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CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: Townsend and Townsend Applicanton Numbers: Us OB/81,813
PRIOR APPLICATION NUMBER: US OB/911,312
PRIOR APPLICATION NUMBER: US OB/912,951
PRIOR APPLICATION NUMBER: US OB/912,951
                                                                                                                                                                                                                                                                                                                        Query Match 93.9%; Score 107; DB 3; Length 129; Best Local Similarity 91.3%; Pred. No. 1e-09; Matches 21; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                      LOCATION: 1.129
OTHER INFORMATION: /note= "TRT motifs from human"
US-08-851-843A-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 ROHLKRVOLRELSEABVROHREA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ROHLKRVOLRDVSEAEVROHREA 23
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Sequence 13, Application US/08974549A

Parent No. 6166178

GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
                                                                                                            STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                    NAME/KEY: Peptide LOCATION: 1..129
                                                                                      amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 114; DB 4; Length 23; 100.0%; Pred. No. 1e-11; tive 0; Mismatches 0; Indels
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Sequence 67, Application US/08851843A
Sequence 67, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Morin, Garegi B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
TITLE OF INVENTION: No. 6093809el Telomerase
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER REALABLE FORM:
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
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NAME: APPLe, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                           NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429
REGISTRENCE/DOCKET NUMBER: 015389-002600US
REPERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 aming acids
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APPLICATION NUMBER: US/08/851,843A
PILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
FILING DATE: 01-OCT-1996
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ROHLKRVOLRDVSEAEVROHREA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RQHLKRVQLRDVSEAEVRQHREA 23
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(415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 100.0
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-851-843A-67
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : NAME/KEY: Peptide

: LCCATION: 1..129

: OTHER INFORMATION: /note= "TRT motifs from human"

US-08-854-050-67
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Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                        PLOUGH APPLICATION DATA

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/644,419

FILING DATE: 18-APR-1997

CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-0CT-1996

CLASSIFICATION: S36
ATTORNEY/AGENT INFORMATION:
NAMME: APPLICATION NUMBER: 36,429

RECISTRATION NUMBER: 36,429

RECISTRATION NUMBER: 36,429

RECISTRATION INFORMATION:
TELEPHONE: (415) 576-0200

INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGRALION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGRH H: 129 amino acids
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FILING DATE: 29-Oct-1999
CLASSIFICATION: <unhclosed-color color colo
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STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
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Patent No. 6309867
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                              FILING DATE: 25
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
US-09-430-323-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
FILING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
FILING DATE: 06-MAY-1997
FILING DATE: 06-MAY-1997
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : LOCATION: 1.129
; OTHER INFORMATION: /note= "TRT motifs from human"
US-08-974-549A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Morin, Gregg B.
APPLICANT: Andrews, William H.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CALIFORNIA
                                                               PRIOR APPLICATION NOTE:

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

PRIOR APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:
NAME: APPLE RANGIPL RANGIPL TOW:
NAME: APPLE RANGIPL TOW:
TELEPHONE: (415) 576-0300

TELEPHONE: (415) 576-0300

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:

TOWN THE REPORT TOWN OF THE POST TOWN O
                                                 UMBER: US 08/915,503
14-AUG-1997
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Patent No. 6261836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 129 amino acids TYPE: amino acid
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Peptide
LOCATION: 1..129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94111
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LENGTH: 129 amino acids TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS-08-974-549A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-912-951-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND TITLE OF INVENTION: HERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: /note= "TRT motifs from human" ; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 91.3%; Pred. No. 1e-09;
Matches 21; Conservative 2; Mismatches 0; Indels
                                                      PILING DATE: 18-APR-1997
PILING DATE: 18-APR-1997
PILING DATE: 18-APR-1997
PILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/44,419
PILING DATE: 10-CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple: Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Felease #1.0, version #1.30 CURRENT APPLICATION NUMBER: US/08/912,951 FILING DATE: 14-AUG-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
APPLICATION NUMBER: US 08/851,843
                       FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States of America ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/08912951
Sequence 13, Application US/08912951
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ROHLKRVOLRDVSEAEVROHREA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Peptide LOCATION: 1..129 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 14-AUG-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-08-912-951-13
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THING DATE: 06-MAY-199

PRING APPLICATION WINGER: US 00/845,017

PRING APPLICATION WINGER: US 00/845,419

CLASSIFICATION WINGER: US 00/724,643

PRING APPLICATION WINGER: US 00/724,643

QUART WINGER: POPICIAL WINGER: US 00/724,643

PRESULT II

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RESULT II

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RESULT III

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RESULT III

PAPLICATION WINGER: OCCIDIN WINGER: ULP APPLICATION WINGER: UND APPLICATION WINGER: UD APPLICATION
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HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
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; OTHER INFORMATION: /note= "protein encoded by clone 712562"
018-08-912-951-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                               SOFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION NUMBER: US 08/854,050
PRIOR APPLICATION DATA:
PPLICATION NUMBER: US 08/851,843
FILING DATE: 09-MAY-1997
CLASSIFICATION TABER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1996
CLASSIFICATION NUMBER: 35,429
FILING DATE: 10-OCT-1996
CLASSIFICATION NUMBER: 36,429
FILING DATE: 10-OCT-1996
CLASSIFICATION NUMBER: 36,429
FILING DATE: 10-OCT-1996
TELLING DATE: 01-OCT-1996
TELLI
   TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC !
TITLE OF INVENTION: THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY. San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 107; DB 4;
Pred. No. 2.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                COUNTRY: United States of America ZIP: 94111
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-08-974-549A-604
; Sequence 604, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ROHLKRVOLRDVSEAEVROHREA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 RÓHLKRVQLRELSEAEVROHREA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 93.9%;
Best Local Similarity 91.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein
                                                                                                                                                                                                CITY: San
STATE: Ca
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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CTHER INFORMATION: /note= "protein encoded by clone 712562"
US-08-974-549A-10
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                                                            FILING DATE: 01-0CT-1996
PRIOR APPLICATION NUMBER: 01-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 09-MAY-1997
PRIOR APPLICATION NUMBER: US 08/911,312
FILING DATE: 09-MAY-1997
PRIOR APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
PRIOR APPLICATION NUMBER: US 08/912,951
PRIOR APPLICATION NUMBER: US 08/912,951
PRIOR APPLICATION NUMBER: US 08/912,951
PRIOR APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-0CT-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-0CT-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-0CT-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-0CT-1997
ATTOMES'/ABRY INFORMATION:
NAME: APPLICATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REFERENCE COCKET NUMBER: 015389-002610US
TELEBEDANE: (415) 576-0200
TELEBETAX: (115) 576-0200
TELEBETAX: (115) 576-0200
TELEBETAX: CHERACTERISTICS:
LENGTH: 259 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
93.9%; Score 107; DB 3;
Best Local Similarity 91.3%; Pred. No. 2.3e-09;
Matches 21; Conservative 2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08912951
Patent No. 6475789
GENERAL INPORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Maranta, Toru
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
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N: 536
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amino acid
                           CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein
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APPLICATION Coch, Thouse R.
APPLICATION INNEMNER, Joseph P.
COMMITTER, CALIFORNIA INNEMNER, JOSEPH P.
APPLICATION INNEMNER, JOSEPH P.
APPLICATION INNEMNER, JOSEPH P.
APPLICATION INNEMNER, JOSEPH P.
APPLICATION INNERNER, JO
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TOTHER INPOMATION: INCHERITION—CHARGE FEACURATION
OTHER INPOMATION: Through of cleavage sequence, recognition
OTHER INPOMATION: Through of cleavage sequence, recognition
OTHER INPOMATION: Requirement for hear mascing process
105-08-74-74-64

OTHER INPOMATION: Sequence for hear mascing process
105-08-74-74-64

OTHER INPOMATION: Annual President introduced by cloming
US-08-74-74-64

OTHER INPOMATION: Annual President introduced by cloming
Marches 21; Conservative 2; Massarches 0; Indels 0; Gaps 0;

APPLICANT CONSERVATION: Annual President Sequence (Sequence Sequence Sequence
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ch 93.9%; Score 107; DB 3;
1 Similarity 91.3%; Pred. No. 5.4e-09;
21; Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: November 12, 2003, 19:53:27 Job time : 11.7044 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ROHLKRVQLRDVSEAEVRQHREA 23
                                                                                                                                                                                                                                                                                                                                                                LENGTH: 530 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1.530
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Protein
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
STREEM STREEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUWIRY: USA ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-007-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
FILING DATE: 25-APR-1997
FILING DATE: 25-APR-1997
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                           278 RQHLKRVQLRELSEAEVRQHREA 300
                                                                                                                                                                                                                                                                                                                              1 ROHLKRVQLRDVSEAEVROHREA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 603, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
                                 318:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 31.
SEQUENCE CHARACTERISTICS:
LENGTH: 515 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                    TOPOLOGY: linear

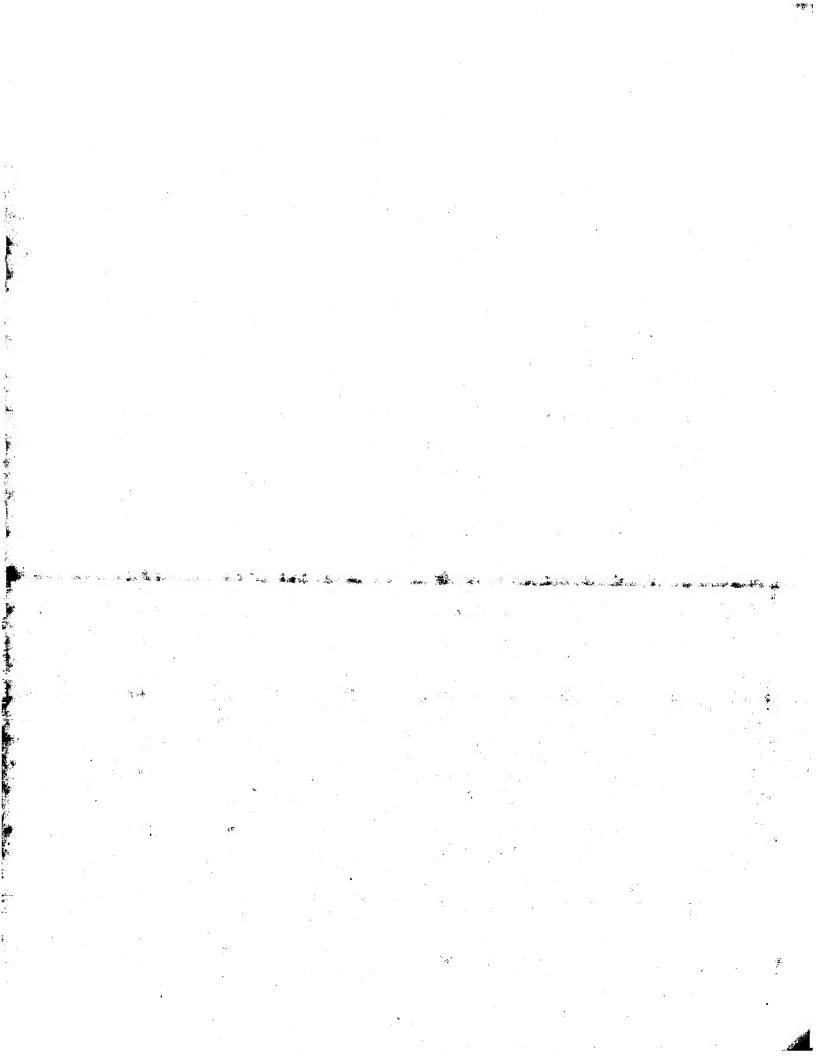
MOLECULE TYPE: protein

US-08-912-951-318
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-08-974-549A-603
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thrombin cleavage sequence, recognition sequence for heart muscle protein kinase, residues introduced by cloning, eight consecutive His residues and hTRT protein fragment."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "fusion protein composed of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glutathione-S-transferase sequence
PRILING DATE: 01-0CT-1997
PRIOR APPLICATION NUMBER: W0 PCT/US97/17618
FILING DATE: 01-0CT-1997
APPLICATION DATA: W0 PCT/US97/17885
FILING DATE: 01-0CT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 16,429
REFERENCE/DOCKET NUMBER: 16,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0300
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 603:
SEQUENCE CHARACTERISTICS:
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Gaps ö

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101, App
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12, App
21, App
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Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Callvin
TITLE OF INVENTION: No. US20020164786A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPER Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Ralease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
RPILOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-AAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 38-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 38-APR-1997
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
              US-10-044-692-10

US-10-294-739-10

US-10-294-778-2

US-10-294-778-2

US-10-294-778-10

US-10-294-778-10

US-10-044-692-318

US-10-044-639-317

US-10-044-639-317

US-10-044-639-317

US-10-044-639-317

US-10-044-639-317

US-10-054-611-101

US-09-643-676-101

US-10-054-611-101

US-10-054-611-101

US-10-054-778-12

US-10-054-611-101

US-10-054-611-101
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STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 113, Application US/09843676; Patent No. US20020164786A1; GENERAL INFORMATION:
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Sequence 113,
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Sequence 114,
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Sequence 67,
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"(gn2_6)ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-766-253-113
US-09-766-253-113
US-10-053-758-113
US-10-054-295-113
US-10-044-611-113
US-09-766-253-114
US-09-766-253-67
US-09-766-253-67
US-09-433-486-67
US-09-766-253-67
US-09-434-486-67
US-10-053-758-67
US-10-054-61-67
US-10-054-61-67
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1 RQHLKRVQLRDVSEAEVRQHREA 23
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Maximum Match 100%
Listing first 45 summaries
                                                                              - protein search, using sw model
                                                                                                                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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CORRESPONDENCE ADDRESS: CARRESPONDENCE ADDRESSE: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                              Indels
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                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTE: CALIFORTIA

COUNTER: CALIFORTIA

ZIP: 94111-3834

COMPUTER READABLE FORM:
COMPUTER FLADABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION S36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 18-APR-1997
CLASSIFICATION S36
PRIOR APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: NIMBER: US 08/724,643
FILING DATE: NIMBER: US 08/724,643
FILING DATE: RADAOLD TIPERCOMMUTION:
NAME: APPLICATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION INFORMATION:
TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-09-766-253-113
                                                                                                                                                                                                                                                                        1 ROHLKRVOLRDVSEAEVROHREA 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 113, Application US/09438486; Publication No. US20030009019A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino
STRANDEDNESS
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; Sequence 113, Application US/09766253
; Sequence 113, Application US/09766253
; Publication No. US20020187471A1
; Publication No. US20020187471A1
; Applicant Cech, Thomas R.
ingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Greeg B.
Harley, Calvin
Harley, Calvin
TITLE OF INVENTION: No. US20020187471A1e1 Telomerase
NUMBER OF SEQUENCES: 171
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MEDIUM TYPE: FOLDAPY disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/766,253

FILING DATE: 19-40-100

RAPLICATION NUMBER: 08/846,017

APPLICATION NUMBER: 08/846,017

APPLICATION NUMBER: 08/846,017

APPLICATION NUMBER: 08/724,643

FILING DATE: 10-70-100

ATORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 36,429

REGISTRATION NUMBER: 05.0000

TELECOMMUNICATION NUMBER: 015389-002920US

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 5.76-0200
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ADDRESSEE Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California
                                                                           NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECHONE: (415) 576-0300
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 23; Conservative 0; Mismatches 0;
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-09-843-676-113
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LENGTH: 23 amino acids
TYPE: amino acid
                                    FILING DATE: 01-OCT-1996
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                                                                  ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
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Lingner, Joachim
Nakamura, Toru
Chaman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INENTION: No. US20030044953A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 23;
           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
CERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
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100.0%; Score 114; DB 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/10/054,295
FILING DATE: 18 Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 113:
                                                  1 ROHLKRVQLRDVSEAEVROHREA 23
                                                                          1 ROHLKRVQLRDVSEAEVRQHREA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ROHLKRVQLRDVSEAEVROHREA 23
                                                                                                                                                                                               Application US/10054295
o. US20030044953A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 23 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415)
        23; Conservative
                                                                                                                                                                                               Sequence 113, Applicat
Publication No. US2003
GENERAL INFORMATION
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                                                                                                                                                                         US-10-054-295-113
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        Matches
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                                                                                                                                 Gaps
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                                                                                        Length 23;
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                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Nakāmura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030032075Alel Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                 ch 100.0%; Score 114; DB 11; Similarity 100.0%; Pred. No. 2.3e-10; 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION S36
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 05-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-053-758-113
                                                                                                                                                                                             1 ROHLKRVOLRDVSEAEVROHREA 23
                                                                                                                                                                                                                                                                                                               Sequence 113, Application US/10053758
Publication No. US20030032075A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (415) 576-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                 MOLECULE TYPE: peptide
linear
                                                                                                     Best Local Similarity
Matches 23; Conserv
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Best Local Similarity
                                       US-09-438-486-113
                                                                                                                                                                                                                                                                        RESULT 4
US-10-053-758-113
TOPOLOGY:
                                                                                 Query Match
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Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
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                                                                                                                                                                                              STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/912,951
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-10-044-692-114
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Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ROHLKRVOLRDVSEAEVROHREA 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                  CITY: San Francisco
                                                                                                         CORRESPONDENCE ADDRESS
                                                                                      SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-044-539-114
                                                                                         NUMBER OF
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                                                                           APPLICANT: Cech, Thomas R.

APPLICANT: Cech, Thomas R.

Lingner, Joachim
Nakamura, Toru
Chaman, Karen B.

Morin, Gregg B.

Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: No. US20030059787Alel Telomerase
NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: AUANOWN-
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
                                                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 113:
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US-10-044-692-114
iS-10-044-692-114, Application US/10044692
; Sequence 114, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INPORMATION:
; APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
; Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ROHLKRVQLRDVSEAEVROHREA 23
           Sequence 113, Application US/10054611
Publication No. US20030059787A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-054-611-113
  US-10-054-611-113
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                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPPY disk

MEDIUM TYPE: RIOPPY disk

MEDIUM TYPE: RIOPPY disk

COMPUTER: 18M PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/843,676

FILING DATE: 26-Apr-2001

CLASSIFICATION DATA:

APPLICATION NUMBER: US/08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/44,419

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INPORMATION:

NAME: Appl.

REGISTRATION NUMBER: 36,429

REGISTRATION NUMBER: 36,429

REGISTRATION NUMBER: 36,429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andrews, William H.

TITLE OF INVENTION: No. US20020187471A1el Telomerase NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California
                    ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                 CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 67, Application US/09766253; Publication No. US20020187471A1 GENERAL INFORMATION:
APPLICANT: Cech, Thomas R. Lingner, Joachim Nakamura, Toru Chapman, Karen B. Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 576-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 67
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-843-676-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-766-253-67
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               DIAGNOSTIC AND
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IITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 67, Application US/09843676
Fatent No. US20020164786A1
GENERAL INFORMATION:
APPLICANT Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Kazen B.
Mozin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020164786A1e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 23;
                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

APPLICATION DATA:

APPLICATION NUMBER: US/10/044,539

FILING DATE: 11-Jan-2002

CLASSIFICATION DATA:

APPLICATION NUMBER: 08/912,951

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/81,419

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

ATTORNEY AGENT INFORMATION:

MAND: AND OPERS ON OPERS US 08/724,643

FILING DATE: 10-OCT-1996
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                                                                                                            Crew LLP
                                                                                               ADDRESSEE: Townsend and Townsend and Crew STREET: Two Embarcadero Center, 8th Floor STREET: San Francisco STATE: California COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 100.0%; Score 114; DB 15; Similarity 100.0%; Pred. No. 2.3e-10; 3; Conservative 0; Mismarrhan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Apple, Randolph T.
EGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
                                   HERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 114:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ROHLKRVQLRDVSEAEVRQHREA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ROHLKRVOLRDVSEAEVROHREA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 576-03 INFORMATION FOR SEQ ID NO: 114:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Simi:
Matches 23; (
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Chapman, Karen
Chapman, Karen
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. US20030032075Alel Telomerase
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 91.3%; Pred. No. 1.6e-08;
Matches 21; Conservative 2; Mismatches 0;
FILING DATE: 12-NOV-1999
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: 356
ATTORNEY AGENT INFORMATION:
NAME: APPLICATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 35,429
REFERENCE/DOCKET NUMBER: 35,620
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAN: (415) 576-0300
TELEPRAN: (415) 576-0300
TELEPRAN: CALBARATICH:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ROHLKRVQLRDVSEAEVROHREA 23
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Publication No. US20030032075A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cech, Thomas R. Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakamura, Toru
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1.129
OTHER INFORMATION:
US-09-438-486-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /note= "TRT motifs from human" SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-418-486-67
Sequence 67, Application US/09438486
Sequence 67, Application US/09438486
Publication No. US20030009019A1
GENERAL INFORMATION:
APPLICANT: Clingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin Harley, Calvin APPLICANT: Applicant: APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US20030009019A1e1 Telomerase
                                                                                       MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                       CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: APPLE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 31,539-002920US
TELEFRANCE/DOCKET NUMBER: 015389-002920US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: United States of America
ZIP: 94111-3834
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California
      COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   California
: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ROHLKRVOLRDVSEAEVROHREA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1.129
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                             ZIP: 94111
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030059787Alel Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenten Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                     NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
93.9%; Score 107; DB 15;
Best Local Similarity 91.3%; Pred. No. 1.6e-08;
Matches 21; Conservative 2; Mismatches 0;
                                                                                                APPLICATION NUMBER: 08/854,050
FILING DATE: «URKNOWN»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-ARR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-ARR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
ATTORNEY/AGENT INFORMATION:
           APPLICATION NUMBER: US/10/054,295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ROHLKRVQLRDVSEAEVROHREA 23
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                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONOR: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO. 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 67, Application US/10054611
Publication No. US20030059787A1
GENERAL INFORMATION:
                                   FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
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Publication No. US20030044953A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030044953A1e1 Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: /note= "TRT motifs from human" SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
WINDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.9%; Score 107; DB 15;
91.3%; Pred. No. 1.6e-08;
live 2; Mismatches 0;
                                   PRIOR DATE: 18-100/053,758
FILING DATE: 18-100/053,758
FILING DATE: 18-1002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US/08/854,017
FILING DATE: 05-MAY-1997
APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: California COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ROHLKRVOLRDVSEAEVROHREA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 RQHLKRVQLRELSEAEVRQHREA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: <Unknown>
                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 67 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 93.9
Best Local Similarity 91.3
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-054-295-67
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Gaps

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Score 107; DB 15; Length 129; Pred. No. 1.6e-08; 1ndels 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1.129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                      NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                 APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: November 12, 2003, 19:55:47 Job time : 19.3711 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ROHLKRVQLRDVSEAEVROHREA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 ROHLKRVOLRELSEAEVROHREA 71
                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                              LENGTH: 129 amino acids TYPE: amino acid
                         FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 93.9%;
1 Similarity 91.3%;
21; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 21; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
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Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 1.6e-08;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Peptide
', LOCATION: 1..129
', OTHER INFORMATION: /note= "TRT motifs from human"
', SEQUENCE DESCRIPTION: SEQ ID NO: 67:
', US-10-054-611-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
                                       APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
PFLLING DATE: 01-007-1996
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FILING DATE: 11-Jan-2002
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/912,951
    APPLICATION NUMBER: 08/854,050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-044-692-13; Application US/10044692; Sequence 13, Application US/1004481; Publication No. US20030096344A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 ROHLKRVOLRELSEAEVROHREA
                                                                                                                                                                                                                                                                                                                                                        LENGTH: 129 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 91.3%;
Matches 21; Conservative ,
                                                                                                                                                                                                                                                                                       TELEFAX: (415) 576-C
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
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Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein

November 12, 2003, 19:43:04; Search time 8.96855 Seconds (without alignments) 246.626 Million cell updates/sec Run on:

US-08-854-050-113

1 RQHLKRVQLRDVSEAEVRQHREA 23 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

hypothetical prote stathmin gene fami hypothetical prote El protein - human hypothetical prote hypothetical prote hypothetical prote aspartokinase II/h carbamoyl-phosphat probable integrase probable integrase transcription elon cobialamin adenosy prophage DLP12 int probable Hflx - My threonyl-tRNA synt telomerase catalyt hypothetical prote probable transposa conserved hypothet hypothetical prote trichohyalin - she probable dxs prote cinesin heavy chai cinesin heavy chai acetyltransferase neurofilament integrase -Description SUMMARIES D81035 E85513 G90662 S26176 G97695 G71061 H87038 B82045 T12528 H81887 RSBPIP A33497 D70505 G87306 E70528 B82097 S15762 184737 A41919 A40691 T03844 Query Match Length DB 107 Result No.

| hypothetical prote | | DNA mismatch repai | | translation initia | transcription fact | hypothetical prote | two-component hybr | hypothetical prote | hypothetical profe | probable transposa | probable ATP/GTP-b | hypothetical prote | hflx protein - Myc | Conserved hypother | conserved hypothet |
|--------------------|------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| S50580 | C28667 | E98107 | AB2587 | B97369 | A47212 | T20767 | AH2085 | T20766 | S22628 | F82016 | G87033 | T35116 | S72938 | A70399 | E69495 |
| | | | | | | | | | | | | | | | |
| ~ | N | N | ~ | 7 | N | N | N | ~ | 7 | 7 | 7 | 7 | 7 | 7 | ~ |
| 688 2 | 844 2 | 857 2 | 913 2 | 913 2 | 1093 2 | 1302 2 | 1707 2 | 1767 2 | 288 2 | 335 2 | 488 2 | 497 2 | 518 2 | 814 2 | 191 2 |
| | | | | | _ | - | _ | _ | | | | | | | |
| | 37.7 844 2 | | | | _ | - | _ | _ | | | | | | | |
| | | | | | _ | - | _ | _ | 37.3 | | 37.3 | 37.3 | 37.3 | 37.3 | 36.8 |

RESULT 1

telomerase catalytic chain - human

N.Alternate names: telomerase reverse transcriptase C;Species: Homo sapiens (man) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999 C;Accession: T03844 R;Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J. Science 277, 955-959, 1997 A;Title: Telomerase catalytic subunit homologs from fission yeast and human. A;Reference number: 215111; MUID:97400623; PMID:9252327

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA A;Residues: 1-1132 <N

A;Residues: 1-1132 <NAK> A;Cross-references: EMBL:AF015950; NID:g2330016; PIDN:AAC51672.1; PID:g2330017 A;Experimental source: kidney

C; Genetics

A,Gene: TRT A,Map position: 5p

Gaps . 0 Query Match 93.9%; Score 107; DB 2; Length 1132; Best Local Similarity 91.3%; Pred. No. 9.6e-08; Matches 21; Conservative 2; Mismatches 0; Indels 0; Indels

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23 1 ROHLKRVQLRDVSEAEVROHREA

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Carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5) large chain NMA0602 [i C, Species: Neisseria meningitidis
C, Species: Neisseria meningitidis
C, Species: Neisseria meningitidis
C, Species: Neisseria meningitidis
C, Species: Noisseria meningitidis
C, Accession: P81979
R, Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
J, Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A, Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A, Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A, Tatus: Preliminary
A, Molecule type: DNA
A, Residues: 1-1071 cPAR>
A, Fresidues: 1-1071 cPAR>
A, Cross-references GB: AL162753; GB: AL157959; NID: G7379120; PIDN: CAB83892.1; PID: G737933

A;Gene: carB; NMA0602 C;Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain; biotin C;Keywords: ligase

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probable integrase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952) C; Beccise: Bscherichia coli (strain O157:H7, substrain RIMD 0509952) C; Beccise: Bscherichia coli (species: Bscherichia coli #sequence_revision 18-Jul-2001 #text_change 17-May-2002 C; Accession: G90662 C; Accessi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AJ235273; GB:AJ235269; NID:g3861237; PIDN:CAA15285.1; PID:g38613
A;Experimental source: strain Madrid E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cobialamin adenosyltransferase (PA1272) [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Status: preliminary
A,Status: preliminary
A,Rolecule type: DNA
A,Rosidues: 1-162 cMAR>
A,Cross-references: EMBL:Z12122; NID:g46345; PIDN:CAA78107.1; PID:g46346
A,Cross-references: EMBL:Z12122; NID:g46345; PIDN:CAA78107.1; PID:g46346
B,Andersson, S.G.B.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark
B,Andersson, S.G.B.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark
B,Andersson, S.G.B.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark
A;Reference number: A71630; MUID:99039499; PMID:9823893
A;Reference number: A71630; MUID:99039499; PMID:9823803
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcription elongation factor greA - Rickettsia prowazekii
NiAlternate names: RP861
C.Species: Rickettsia prowazekii
C.Species: Rickettsia prowazekii
C.Decies: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 03-Nov-2000
C.Accession: 226176; E71648; S21472
R.Marks, G.L.; Wood, D.O.
Nucleic Acids Res. 20, 3785, 1992
A.Title: Nucleotide sequence of the Rickettsia prowazekii greA homolog.
A.Ricketsion: 226176
A.Accession: 226176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 162;
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C;Superfamily: transcription elongation factor greb
C;Keywords: DNA binding; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.1%; Score 48; DB 2;
47.6%; Pred. No. 7.1;
iive 5; Mismatches '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 QHLKRVQLRDVSE--AEVRQH 20
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KHLKHVERKKISEDIAEAREH 40
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Query Match
Best Local Similarity 47.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Gene: EC80271
C.Superfamily: phage P22 integrase
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Matches, 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
R;Tettellin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.P.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
A;Authors: Grandi, G.; Sun, L.; Sanith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Reference number: A81000; MUID:2017575; PMID:10710307
A;Reference number: A81000; MUID:2017575; PMID:10710307
A;Retus: preliminary
A;Molecule type: DNA
A;References: GB-AE002535; GB:AE002098; NID:g7227103; PIDN:AAF42189.1; PID:g722711
A;Crose-references: GB-AE002535; GB:AE002098; NID:g7227103; PIDN:AAF42189.1; PID:g722711
A;Experimental source: serogroup B, strain MC58
C;Generics
C;Generics
A;Gene: NMB1855
C;Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain; biotin
C;Keywords: ligase
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A;Residues: 1-324 -STO>
A;Cross-references: GB:AE005174; NID:g12513018; PIDN:AAG54569.1; GSPDB:GN00145; UWGP:203
A;Experimental source: strain O157:H7, substrain EDL933
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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, atuler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Article: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A885480; MUID:21074935; PMID:11206551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
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                                      Length 1071;
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                                                                                                          3; Indels
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ilarity 33.3%; Pred. No. 9;
Conservative 7; Mismatches 4;
                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 46.7%; Pred. No. 14;
Matches 14; Conservative 3; Mismatches
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                                      Score 52.5; DE
Pred. No. 11;
2; Mismatches
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                                                                                                                                                                                                                                                          495 KRIAQLLDVKEKEVREHR 512
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                                                                                                                                                                                      S KRV-QLRDVSEAEVROHR 21
                                             46.1%;
nilarity 66.7%;
Conservative 2
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Matches 10; Conserva
                                             Query Match
Best Local Similarity
Matches 12; Conserva
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A,Status: preliminary
A,Molecule type: DNA
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A;Gene: intH
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RESULT 5

Gaps

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hypothetical protein dxs [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: H87038
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R;Cole, S.T.; Eiglmeier, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, eam, M.A.; Butherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Attle: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-643 <STO>
A;Cross_references: GB:AL450380; NID:g13093053; PIDN:CAC31419.1; GSPDB:GN00147
                                                                A;Map position: 3
A;Introns: 52/3; 87/3; 129/2; 162/1; 197/2; 280/3; 393/3; 538/3
                                                                                                                                                                                            Score 47; DB 2;
Pred. No. 38;
                                                                                                                                                                  41.2%; Scor.
42.1%; Pred. No. 50,
... 4; Mismatches
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Pred. No.
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QHLSQQQLRDLA-ABIRELLVHKVA 35
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C;Superfamily: hypothetical protein C2814
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374 QSHVTNAQIRDAKRAEMRQ 392
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1 Similarity 48.0%;
12; Conservative 6
                                                                                                                                                                                    Query Match
Best Local Similarity 42.15
Matches 8; Conservative
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Best Local Similarity
Matches 11; Conserv
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A; Molecule type: DNA
                              A; Gene: CESP: T04C9.6
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                                                                    Rigodoner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2313-2328, 2001
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2313-2328, 2001
A; Teference number: A97359, MuID:21608551; PMID:11743194
A; Accession: G97695
A; Accession: G97695
A; Accession: G97695
A; Mesidues: 1-221 <KUR>
A; Molecule type: DNA
A; Residues: 1-221 <KUR>
A; Molecule type: DNA
A; Gene: AGR C_5090
A; Map position: circular chromosome
C; Superfamily: Escherichia coli cob(I) alamin adenosyltransferase coba
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A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Reference number: A1000; MUID:98344137; PMID:9679194
A;Reference number: A1000; MUID:98344137; PMID:9679194
A;Reference number: A1000; MUID:98344137; PMID:9679194
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-270 cKAW>
A;Residues: 1-270 cKAW
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C;Species: Caenorhabditis elegans
C;Accession: T25859
R;Favello, A.
Submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid T04C9.
A;Reference number: Z20101
A;Reference number: Z20101
A;Reference number: Z20101
A;Residues: T55859
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-568 -FAV>
A;Cross-references: EMBL:UB0955; PIDN:AAB38104.1; GSPDB:GN00021; CESP:T04C9.6
C;Genetics:
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C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
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G71061
G71061
G71061
CSPECIES: PYPOCOCCUS HORIKOSHII
CSPECIES: PYPOCOCCUS HORIKOSHII
CSPECE: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
CSACCESSION: G71061
R.Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamot
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41.2%; Score 47; DB 2; Length 221;
Best Local Similarity 38.9%; Pred. No. 14;
Matches 7; Conservative 6; Mismatches 5; Indels
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Pred. No. 17;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 QHLKRVQLRDVSEABV-----RQHRE 22
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14 ERAMTRDISDSEAERHRQ 31
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1 Similarity 37.0%;
10; Conservative
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Matches 10; Conserv
                                                   Accession: G97695
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Gaps

4 ;

Length 643 3; Indels

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DB

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RiHeidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; WUID:20406833; PMID:10952301
          - Vibr
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1.803 <HEI>
A;Cross-references: GB:AE004135; GB:AE003852; NID:g9657289; PIDN:AAF95825.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C, Superfamily: thra bifunctional enzyme; aspartate kinase homology; homoserine dehydroge
aspartokinase II/homoserine dehydrogenase, methionine-sensitive VC2684 [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ï
                                C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: B82045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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1;

Gaps

6

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A.Residues: 1-387 <BLAT>
A;Cross-references: GB:AE000159; GB:U00096; NID:g1786739; PIDN:AAC73638.1; PID:g1786748
A;Experimental source: strain K-12, substrain MG1655
A;Cross-references: GB:X04052; NID:g15641; PIDN:CAA27685.1; PID:g15642
C;Genetics:
A;Gene: int
C;Superfamily: phage P22 integrase
C;Keywords: DNA integration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 387;
                                                                                                       Length 387;
                                                                                                                                         Indels
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                                                                                                            DB 1;
                                                                                                         Score 45.5; DB Pred. No. 43; 7; Mismatches
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Pred. No. 43;
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                                                                                                                                                                                             2 QHLKRVQLRDVSEAEV-----RQHRE 22
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                                                                                                          39.9%;
illarity 30.0%;
Conservative 7
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Best Local Similarity 33.3%;
Matches 8; Conservative
                                                                                                                         Local Similarity
tes 9; Conserv
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Matches
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A)Experimental source: serogroup A, strain Z2491
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable transposase for IS1106A3 NMA1199 [imported] - Neisseria meningitidis (strain 22 probable transposase for IS1106A3 NMA1199 [imported] - Neisseria meningitidis (strain 22 procession: Nay-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C;Accession: H81887
R;Parkhill, J; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000 A;Reference number: A81775; MUD:2022556; PMID:10761919 Asseria menigitidis 22491. A;Accession: H81887
                                                                                             hypothetical protein DKFZp434N093.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #Bequence_revision 23-Jul-1999 #text_change 23-Jul-1999
C;Date: 23-Jul-1999 #Bequence_revision 23-Jul-1999
C;Accession: T12528
R;Mambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
R;Mambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
R;Mambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
R;Accession: T17228
A;Reference number: Z17524
A;Reterence number: Z17528
A;Reterence preliminary
A;Molecule type: mRNA
A;Residues: 1-745 <WAM>A;Residues: 1-745 <WAM>A;Residues: Generices: EMBL:AL080144
A;Experimental source: adult testis; clone DKFZp434N093
C;Genetics:
A;Note: DKFZp434N093.1
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RQHLKEHRLQDGIMRKACRNRPLSEAQTKRNR 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45.5; DB;
Pred. No. 36;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        Score 46;
Pred. No.
                            331 QHLQRVQLQPLTYEAQPDQYR 351
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412 KHVRRVRGREVSPSDVRE 429
                                                                                                                                                                                                                                                                                                                                                                                                                                       2 QHLKRVQLRDVSEAEVRQ 19
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                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Gene: NMA1199
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RSBPIP
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                                                                                 RESULT 12
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Gaps

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Indels

us-08-854-050-113.rsp

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

November 12, 2003, 19:41:59 ; Search time 4.77358 Seconds (without alignments) 226.583 Million cell updates/sec Run on:

US-08-854-050-113

114 1 RQHLKRVQLRDVSEAEVRQHREA 23 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

127863

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | | O14746 homo sapien | m snm | | neisseria | | | | 8 | P04890 bacteriopha | Q9aax8 caulobacter | P54682 dictyosteli | _ | | | ٠. | P33176 homo sapien | | P22793 ovis aries | | | | P10564 streptococc | P28738 mus musculu | | | Q28270 canis famil | | | Q9x6w9 aquifex pyr | | P43668 salmonella | | Q04855 azorhizobiu |
|-----------|-----------------------|--------------------|------------|------------|------------|------------|------------|-----------|------------|--------------------|--------------------|--------------------|-----------|------------|-----------|------------|--------------------|------------|-------------------|------------|-----------|------------|--------------------|--------------------|------------|------------|--------------------|------------|------------|--------------------|-----|-------------------|-----|--------------------|
| SUMMARIES | ID | DC; | TERT MOUSE | CARB_NEIMA | CARB_NEIMB | GREA_RICPR | TTC4_HUMAN | DXS_MYCLE | INTD_ECOLI | VINT_BPP22 | SYT_CAUCR | D7_DICDI | DXS_MYCTU | YHZ7_YEAST | NFM_CHICK | KF5C_HUMAN | KINH_HUMAN | KINH_MOUSE | TRHY_SHEEP | STN4_XENLA | VE1_HPV49 | YEQ7_YEAST | HEXA_STRPN | KF5C_MOUSE | TMF1_HUMAN | TRA6_NEIMB | CD34_CANFA | GREA_RICCN | SODF_AQUAE | | | UXUA_SALTY | | YNTC_AZOCA |
| | DB | - | П | Н | ~ | ~ | ~ | Н | - | н | - | | | н | - | | -1 | H | - | Н | - | ~ | | | | | | | -1 | гH | | | 7 | - |
| | Query Match Length | 1132 | 1122 | 101 | 1071 | 162 | 387 | 643 | 387 | 387 | 655 | 850 | 638 | 763 | 857 | 957 | 963 | 963 | 1549 | 185 | 609 | 688 | 844 | 926 | 1093 | 288 | 389 | 162 | 212 | 212 | 386 | 394 | 637 | 735 |
| عد | Query | r | 2 | 46.1 | Š. | 42.1 | ä | 4 | ٠. ص | φ. | 6 | 6 | φ. | 38.6 | ω. | ω. | 38.6 | œ · | 8 | 7. | ζ. | | <u>,</u> | 37.7 | | ζ. | ۲. | ė. | 36.8 | ė | ė. | 36.8 | ė. | 36.8 |
| | Score | 10 | 7 | 52.5 | 52 | 48 | 47 | 4 | 'n. | 2 | | S. | 45 | 44 | 44 | | 44 | 44 | 43.5 | | | 43 | 43 | 43 | 4 | N | 42.5 | 42 | 42 | 42 | 42 | 42 | 42 | 42 |
| | Result No. | н | 7 | m | 4 | ហ | 9 | 7 | 80 | ָס | 30 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 23 | 22 | 53 | 5.4 | 25 | 56 | 27 | 28 | 29 | 30 | 31 | 32 | 33 |

| Q99zn6 homo sapien P38249 saccharomyc Q13505 homo sapien P75537 mycoplasma P52127 escherichia P4198 caenorhabdi O75921 homo sapien Q9esd7 mus musculu Q9esd7 mus musculu Q99240 caenorhabdi P55466 rhizobium s Q9nyw3 homo sapien O69232 buchnera ap |
|--|
| NTT5 HUMAN IF7A YEAST MIX1_HUMAN WIX1_HUMAN YEJU_ECOLI TCPA_CABEL DYSF HUMAN DYSF_MOUSE YQAZ_CABEL X1C_RISN T2R7_HUMAN RPOA_BUCAP |
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| 736 964 317 417 518 549 2080 2081 194 194 230 318 |
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ALIGNMENTS

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Query Match
Best Local S
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between the Swiss Institute of Bioinformatics and the EMBL outstation-
the Buropean Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                      MINN; JC.1.V.V., C:telomere; TAS.
GO; GO:0005696; C:telomere; TAS.
GO; GO:0003721; F:telomeric template RNA reverse transcriptas. . .; TAS.
GO; GO:0007003; P:telomere binding; TAS.
InterPro; IPR000477; RVTse.
InterPro; IPR003545; Telomerase_RT.
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                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
                                                                                                                                                                                                                                                      Pfam; PF00078; rvt; 1.
PRINTS; PR01365; TELOMERASERT.
Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homolog.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL
'THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT
ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98393668; PubMed=9724727;
Martin-Rivera L., Herrera E., Albar J.P., Blasco M.A.;
"Expression of mouse telomerase catalytic subunit in embryos and
adult tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=98241176; PubMed=9582020;
MEDLINE=98241176; PubMed=9582020;
MEDLINE=98241176; PubMed=9582020;
MEDLINE=98241176; PubMed=988.A., Allsopp R.C., Chin L., Morin G.B., DePinho R.A.;
MEDLINE=98241176; PubMed=988.A., Morin G.B., DePinho R.A.;
Medoelpoment, differentiation and proliferation.";
Morcogene 16:1723-1730(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Partial sequence of Mus musculus telomerase catalytic subunit
                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                  93.9%; Score 107; DB 1; Length 1132; 91.3%; Pred. No. 4e-08; cive 2; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                516 516 D -> G (IN REF. 2).
1132 AA; 126996 MW; 94E35469C4CA33A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 95:10471-10476(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1122 AA
                                                                                                         1 ROHLKRVQLRDVSEAEVROHREA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 550-616 FROM N.A.
                                                                                          EMBL; AF015950; AAC51672.1; -.
EMBL; AF018167; AAC51724.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drissi R., Cleveland J.L.;
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 91.33
Matches 21, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TERT MOUSE ST
070372; 035432;
30-MAY-2000 (Rel.
                                                                                                                                                                                                                                                                                           DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subunit).
                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase, RNA-directed DNA polymerase, Telomere, Nuclear protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Z2491 / Serogroup A / Serotype 4A;
STRAIN=Z2491 / Serogroup A / Serotype 4A;
MEDLINE=20225556; PubMed=10761919;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
Riee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Klee S.R., Davis P., Devlin K., Peltwell T., Handin N., Holroyd S.
Davies R.M., Davis P., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthase large chain)
CARB OR NMAG602.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis (serogroup A).
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales;
Neisseriaceae, Neisseria.
                     SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
-!- SUBUNIT: Interacts with PINX1 (By similarity).
-!- SUBCELIULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
TELOMERASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 75; DB 1; Length 114/
Pred. No. 0.0023;
2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - 553 553 I -> V (IN REF. 3).
1122 AA; 127977 MW; F85266905DD6558C CRC64;
SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1071 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        601
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InterPro; IPR003545; Telomerase_RT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ROHLKRVOLRDVSEAEVROHRE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF051911; AAC09323.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF073311; AAC34821.1; -. EMBL; AF029235; AAB84200.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01365; TELOMERASERT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:1202709; Tert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00078; rvt; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=MCS8 / Serogroup B;
MEDLINE=20175755; PubMed=10710307;
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                           R HAMAP; MF 01210; - 1.

R INTERPRO; IPR006275; Cara_L_glu.
R INTERPRO; IPR005481; CPase_L_L.
R INTERPRO; IPR005481; CPase_L_L.
R INTERPRO; IPR005481; CPase_L_L.
R INTERPRO; IPR005481; CPase_L_D.
R INTERPRO; IPR004562; MGS 1Tke.
R INTERPRO; IPR004562; MGS 1Tke.
R INTERPRO; IPR004562; MGS 1Tke.
R Ffam; PF002786; CPSase_L_D.D.; 2.
R Ffam; PF002142; MGS, ITke.
R Ffam; PF002142; MGS, ITke.
R Ffam; PF002142; MGS, IT.
R FAMINTS; PR00099; CPSASE_L_L.
R FAMINTS; PS000866; CPSASE_L, I.
R PROSITE; PS000866; CPSASE_L; I.
R ROSITE; PS000866; CPSASE_L; I.
R ROSITE; PS000866; CPSASE_L; I.
R PROSITE; PS000866; CPSASE_L; I.
R PROSITE; PS000866; CPSASE_L; I.
R POMAIN.
I 403 CCARBOXPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CARB OR NMB1855.
NB1855-IN MB1855:
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (POTENTIAL).
ATP (POTENTIAL).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73B39CBD06729974 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1071 AA
-!- SIMILARITY: BELONGS TO THE CARB FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117419 MW;
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495 KRIAQLLDVKEKEVREHR 512
                                                                                                                                                   EMBL; AL162753; CAB83892.1; -.
PIR; F81979; F81979.
HSSP; P00968; 1A9X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 KRV-QLRDVSEAEVROHR 21
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Best Local Similarity 66.79,
Thes 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               548
930
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NP_BIND
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Q9JXWB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ï
Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Felischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parkes D.S., Blair E., Cittone H., Clark B.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C., "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGRFAMS; TIGRO1303; CECTOR CPASE 1; 1.
PROSITE; PS00866; CPSASE 1; 1.
PROSITE; PS00867; CPSASE 1; 1.
ATP-binding; Manganese; Complete proteome.

CARBOXTPHOSPHATE SYNTHETIC DOMAIN.
DOMAIN 404 548 OLIGOMERIZATION DOMAIN.
DOMAIN 549 930 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
DOMAIN 1071 ALLOSTERIC DOMAIN.
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SIMILARITY).
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ATP (POTENTIAL).

MANGANESE I (BY SIMILARITY).

MANGANESE I AND 2 (BY SIMILAR

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).
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Pred. No. 5.9;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 OHLKR-----VQLRDVSEAEVRQHREA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAMAR, MF 01210; -; 1.
InterPro; IPR006275; CarA L glu.
InterPro; IPR005483; CPase L.
InterPro; IPR005489; CPase L.
InterPro; IPR005480; CPase L. D3.
InterPro; IPR005481; CPase L. D3.
InterPro; IPR005481; CPase L. N.
InterPro; IPR004362; MGS_IIke.
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                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE002535; AAF42189.1; -.
PIR; D81035; D81035.
HSSP; P00968; 1A9X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00289; CPSase L Dain; Pfam; PF02786; CPSase L D2; 2. Pfam; PF02787; CPSase L D3; 1. Pfam; PF02142; MGS; 1.
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1071 AA; 117375
                                                                                                                                Science 287:1809-1815(2000)
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nes 14; Conservative
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TIGREAMS; TIGR01369; CPS
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548
1071
210
354
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303
285
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NP_BIND
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Matches
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Interery
Interery
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Interery
Pfam, PR01272; GreA_GreB; 1.
Pfam, PR01272; GreA_GreB N; 1.
Probom; PD004918; GreA_GreB; 1.
TICREAMS; TIGRO1462; GreA; 1.
TICREAMS; TIGRO1462; GreAB 1; 1.
PROSITE; PS00819; GREAB 1; 1.
PROSITE; PS00810; GREAB 2; 1.
Transcription regulation; Onlied coil; Complete proteome.
Transcription regulation; Onlied Coil.
Transcription regulation; DMA-binding; Coiled CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 396:113-140(1998).

Interest 196:1133-140 (1998).

In Constant of the property of trapping a seriesting sites in DNA have the property of trapping a certain fraction of sites in DNA have the property of trapping a certain fraction of elongating RNA polymerases that pass through, resulting in locked ternary complexes. Cleavage of the nascent transcript by cleavage factors such as grea A or grea allows the resumption of elongation from the new 3'terminus. Grea releases sequences of 2 to 3 nucleotides (By similarity).

In SIMILARITY: BELONGS TO THE GREA/GREB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=9901999; PubMed=9823893; Andersson J.O., Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Elixsson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of mitochondria.";
                                                                                                                                                                                                                                                                                                               Marks G.L., Wood D.O.; "Nucleotide sequence of the Rickettsia prowazekii greA homolog."; Nucleic Acids Res. 20:3785-3785(1992).
                                  01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transcription elongation factor greA (Transcript cleavage factor
                                                                                                                                                           Rickettsia prowazekii.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.1%; Score 48; DB 1; Length 162; 47.6%; Pred. No. 3; ive 5; Mismatches 4; Indels
162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ238273; CAA15285.1; -.
PIR; S26176; S26176.
HSSP; P21346; 1GRJ.
HAMAP; MF_00105; -; 1.
InterPro; IPR006359; GreA.
InterPro; IPR0061437; GreA_GreB.
                                                                                                                                                                                                                                                                                  STRAIN=Madrid E;
MEDLINE=92350688; PubMed=1641348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z12122; CAA78107.1; -. EMBL; U02878; AAB81401.1; -.
    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Madrid E;
                                                                                                                                                                                                                       NCBI TaxID=782;
                                                                                                                                           GREA OR RP861.
    RICPR
                        P27640
        GREA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUB=CEVILX;

WEDLINE=21388257; PubMed=12477932;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Straubberg R.D., Colling F.S., Wagner L., Shemen C.R., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Expleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Rownstein M.J., Usdin T.B., Porblyvki S., Carninci P., Prange C.,

B Rohas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., And E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

B Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Rutterfield Y.S.N., Krzywinski M.I., Schliska U., Smailus D.E.,

R Generatical M.S., Marnander M., Marra M.A.;

R Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99134293; PubMed=9933562;
Su G., Roberts T., Cowell J.K.;
"TTC4, a novel human gene containing the tetratricopeptide repeat and
mapping to the region of chromosome lp31 that is frequently deleted in
sporadic breast cancer.";
Genomics 55:157-163(1999).
                                                                                                                                                                                                                                                                                                Eukaryoca, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mao Y.M., Xie Y., Zheng Z.H.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                  TTC4 HUMAN STANDARD; PRT; 387 AA.
095801; Q9H312;
30-MAY-2000 (Rel. 39, Created)
15-FB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Tetratricopeptide repeat protein 4 (My044 protein)
                                                                                                                                387 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO: 0008181; F:tumor suppressor; TAS. GO; 0007048; P:oncogenesis; TAS. InterPro; IPR001440; TPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human and mouse cDNA sequences.";
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KHLKHVERKKISEDIAEAREH 40
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EMBL; AF063602; AAG43161.1; -.
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                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Fetal brain;
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                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
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10; Conservative

** Matches

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Gaps

5

us-08-854-050-113.rsp

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or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                    ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                             Query Match
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P24218;
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                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                ö
                       TPR 1.
TPR 2.
TPR 2.
TPR 3.
T -> S (IN REF. 1).
K -> I (IN REF. 1).
PUNLUYFEDEDRAELYRYPAKSTILLQULQHQRYFVKALTP
AFLVCVGSSPFCKNPILGRKCYQIR -> LIWRSTLRMFT
GQNYTGCLPRAPCYRFYSTRGTL (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- FUNCTION: Catalyzes the acyloin condensation reaction between C atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to yield 1-deoxy-D-xylulose-5-phosphate (DXP) (By similarity)
-!- CATALYTIC ACTIVITY: Pyruvate + D-glyceraldehyde 3-phosphate = 1-deoxy-D-xylulose 5-phosphate + CO(2).
-!- COPACTOR: Binds 1 thiamine pyrophosphate per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Davien R., Davies R.M., Davin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Ruther S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Barrell B.G.; Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       step
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: Homodimer (By similarity).
-!- SIMILARITY: Belongs to the transketolase family. DXPS subfamily.

    similarity).
    PATHWAX: Nonmevalonate terpenoid biosynthesis pathway; first st
    PATHWAY: Biosynthetic pathway to thiamine and pyridoxol; first

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                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium leprae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                   41.2%; Score 47; DB 1; Length 387; llarity 42.1%; Pred. No. 11; Conservative 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                         1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7) (1-deoxyxylulose-5-phosphate synthase) (DXP synthase) (DXPS).
                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Smith D.R., Robison K.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                              20EC8CC3F78A8233 CRC64;
                                                                                                                                                                                                                                                                                                                 15-UUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                               643 AA.
                                                                                                                                                                              7; Mismatches
                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21128732; PubMed=11234002;
                                                                                                                                                                                                                     197 LKRIEQRDVRKANLKEKKE 215
                                                                                                                                                                                                     4 LKRVQLRDVSEAEVROHRE 22
                                                                                                                           387 AA; 44692 MW;
                                                                                                                                                                                                                                                                                              STANDARD;
                         1112
150
184
47
47
165
Pfam; PF00515; TPR; 3.
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                                                                                                                                     Query Match
Best Local Similarity
           Repeat, TPR repeat
REPEAT 79
REPEAT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1769;
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Q50000;
                                               REPEAT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                           SEQUENCE
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SEQUENCE FROM N.A.
Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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"Nucleotide sequence of the region encompassing the int gene of a
"typtic prophage and the dna Y gene flanked by a curved DNA sequence
of Escherichia coli K12.";
                    REMBL; ALS633920; CGZ31419.1; -
REMBL; ALS633920; CGZ31419.1; -
R PIR; H87038; H87038.
R Lepromas, MI1038; -
R Lepromas, MI1038; -
R InterPro; IPR005477; Dxs.
R InterPro; IPR005476; Transketolase_CR.
R InterPro; IPR005474; Transketolase_CR.
R InterPro; IPR005474; Transketolase_CR.
R InterPro; IPR005474; Transketolase_N.
R Pfam; PF02779; transket_pyr; 1.
R PGSTTE; PS00801; TRANSKETOLASE_1; 1.
R PROSITE; PS00801; TRANSKETOLASE_2; 1.
R Transferase; Flavoprotein; Thiamine pyrophosphate;
W ISOPENE biosynthesis; Complete proteome.
Q SEQUENCE 643 AA; 68862 MW; 2C86C884ABCAA00B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=K12 / MG1655;
BIBLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lindsey D.F., Mullin D.A., Walker J.R.; "Characterization of the cryptic lambdoid prophage DLP12 of Escherichia coli and overlap of the DLP12 integrase gene with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 643;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 21, Last sequence update)
Prophage DLP12 integrase (Prophage QSR' integrase).
BROBERICHIA COLI.
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19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.2%; Scor.
48.0%; Pred. No. 1>,
... 6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 OHLSOQQLRDLA-AEIRELLVHKVA 35
EMBL; U15181; AAA62954.1; ALT_INIT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=K12;
MEDLINE=90036709; PubMed=2553674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=90220507; PubMed=2183007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriol. 171:6197-6205(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterobacteriaceae; Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 277:1453-1474 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 48.0
Matches 12; Conservative
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THRS OR CC0464.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"The completed (DEC-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: INTEGRASE IS NECESSARY FOR INTEGRAPION OF THE PHAGE INTO THE HOST GENOME BY SITE-SPECIFIC RECOMBINATION. IN CONJUNCTION WITH EXCISIONASE, INTEGRASE IS ALSO NECESSARY FOR EXCISION OF THE
Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
"Sequence of minutes 4-25 of Escherichia coli.";
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: INTEGRASE FROM THE CRYPTIC LAMBDOIC PROPHAGE DLP12.
INTEGRASE IS NECESSARY FOR INTEGRATION OF THE PHAGE INTO THE HOST GENOME BY SITE-SPECIFIC RECOMBINATION. IN CONJUNCTION WITH EXCISIONASE, INTEGRASE IS ALSO NECESSARY FOR EXCISION OF THE PROPHAGE FROM THE HOST GENOME.
--- SIMILARITY: BELONGS TO THE "PHAGE" INTEGRASE FAMILY. VERY HIGH, TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Leong J.M. P. Landy A.;
Susskind M.M. Landy A.;
Structural and regulatory divergence among site-specific "structural genes of lambdoid phage.";
J. Mol. Biol. 189:603-616(1986).
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
P22-like viruses.
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HSSP; P2142; IAIH.
HSSP; P2142; IAIH.
EcoGene: E010507; intD.
Enderero; IPR002104; Phage_integrase.
InterPro; IPR005104; Phage integrase; I.
Pfam; PP00589; Phage integrase; I.
DNA recombination; DNA integration; Complete proteome.
TRANSIENT COVALENT LINKAGE TO I STRAND CLEAVAGE AND REJOINING
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45.5;
Pred. No. 18
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                                                                                                                                                                                                                                                                                                                                                                     BACTERIOPHAGE P22 INTEGRASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.9%;
33.3%;
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EMBL; X51662; CAA35974.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M31074; AAA65483.1; -.
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Best Local Similarity 33.3
Matches 8; Conservative
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(Rel. 05, I
(Rel. 40, I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10754;
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P04890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-1987
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ntegrase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOT THE SERVICE COURT SERVICE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
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SEQUENCE FROM N.A.

STRAIN=ATCC 19089 / CB15;

XMEDLINE=21173698; PubMed=11259647;

MEDLINE=21173698; PubMed=11259647;

ME Ender W.C., Feldblyum T.V. Laub M.T., Paulsen I.T., Nelson K.E.,

A Nierman W.C., Feldblyum T.V., Laub M.T., Phidden J.R.,

Beisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Detocka I., Nelson W.C., Newton A., Stephens C., Phidden N.D., Ely B.,

Rolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

A College S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

"Complete genome sequence of Caulobacter crescentus.";

"Complete ATVITY: ATP + L-threonine + ERNA(Thr) = AMP +
PROPHAGE FROM THE HOST GENOME.
SIMILARITY: BELONGS TO THE "PHAGE" INTEGRASE FAMILY. VERY HIGH, TO
E.COLI CRYPTIC LAMBDOIC PROPHAGE DLP12 INTEGRASE (INTD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSIENT COVALENT LINKAGE TO DNA DURING STRAND CLEAVAGE AND REJOINING (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Threonyl-tRNA synthetase (EC 6.1.1.3) (Threonine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diphosphate + L-threonyl-tRNA(Thr).
-!- COFACTOR: Binds 1 zinc ion per subunit (By similarity)
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           387 AA; 44782 MW; 5E4EBA51B3B30802 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 45.5; DE pred. No. 18; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        655 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 QHLKRVQLRDVSEAEV------RQHRE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro, IPR002104; Phage integrase. Pfam; PF00589; Phage integrase; 1. DNA recombination; DNA integration. ACT SITE 349 349 TRANSIEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X04052; CAA27685.1; -.
EMBL; AF217253; AAF75002.1; -
PIR; C24253; RSBPIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 30.0
nes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=155892;
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STRAIN=H37Rv;
                                                                                                                                                                      DXS_MYCTU
007184;
                           SEQUENCE
                                                  Query Match
      DOMAIN
                                                                       Matches
                                                                                                                                                          DXS_MYCTU
                                                                                            Š
                                                                                                                d
                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                           HAMAP; ME 00184; -; 1.

R InterPro; IPR004154; HGTP anticodon.

R InterPro; IPR002134; HGTP anticodon.

R InterPro; IPR002134; tRNA-synt_2b.

R InterPro; IPR0021329; HGTP anticodon; 1.

R fam; PP03129; HGTP anticodon; 1.

R fam; PP03129; HGTP anticodon; 1.

R Fam; PP03129; HGTP anticodon; 1.

R Pfam; PP03129; HGTP anticodon; 1.

R RINTS; PR01047; TRNASYNTHTHR.

R RINTS; PR01047; TRNASYNTHTHR.

R RIGRAMs; TIGR00418; thrS; 1.

R PROSITE; PS50862; AA TRNA LIGASE II; 1.

R Maincacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Amincacyl-thinding; Zinc; Complete protecome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- DEVELOPMENTAL STAGE: EXPRESSED SPECIFICALLY IN THE PRESPORE CELLS.
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=AX3;
MEDLINE=95080502; PubMed=7988791;
MEDLINE=95080502.
Magarwal A., Sloger M.S., Oyama M., Blumberg D.D.;
"Analysis of a novel cyclic Amp inducible prespore gene in
Dictyostelium discoideum: evidence for different patterns of cAMP
                                                                                                                                                                                                                                  (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
CAMP-INDUCIBLE PRESPORE PROTEIN D7
POLY-GLN.
                                                                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                                                                                       39.9%; Score 45.5; DB 1; Length 655; 50.0%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                  73719 MW; BB75D312CC887799 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                  ZINC (CATALYTIC)
ZINC (CATALYTIC)
ZINC (CATALYTIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cAMP-inducible prespore protein D7 precursor
                                                                                                                                                                                                                                                                                                                                                                                                               850 AA
                                                                                                                                                                                                                                                                                                               3; Mismatches
 send an email to license@isb-sib.ch)
                                                                                                                                                                                                                        CATALYTIC
                                                                                                                                                                                                                                                                                                                                                   237 HLKRIE-----EAEKRDHRK 251
                                                                                                                                                                                                                                                                                                                                   3 HLKRVQLRDVSEAEVRQHRE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Differentiation 57:151-162(1994)
                      AE005719; AAK22451.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, U25143, AAA73514.1; -.
DictyDb, DD02038; -.
Sporulation, Signal.
                                                                                                                                                                                                                                                                                                             10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                            391
517
                                                                                                                                                                                                                                  340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24
850
475
                                                                                                                                                                                                                                340
391
317
517
655 AA;
                                            P00955; 1EVL.
CC0464; -.
                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                        248
                                  G87306
                                                                                                                                                                                                                                                                                                                                                                                                             D7_DICDI
P54682;
                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                        Query Match
                     EMBL;
                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                   Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CDC 1551 / Oshkosh,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harris D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway, first step.
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBŪNIT: Homodimer (By similarity).-!- SIMILARITY: Belongs to the transketolase family. DXPS subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Esjameier K., Gas S., Bary C.E. III. Tekaia F., Davies R., Davies R., Devlin K., Feltwell T., Gentles S., Hamin N., Holroyd S., Hornby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-deoxy-D-xylulose-5-phosphate (DxP) (By similarity).
-!- CATALYIC ACTIVITY: Pyruvate + D-glyceraldehyde 3-phosphate deoxy-D-xylulose 5-phosphate + CO(2).
-!- COFACTOR: Binds 1 thiamine pyrophosphate per subunit (By similarity).
                                                                                                                                                                .;
-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7) (1-deoxyxylulose-5-phosphate synthase) (DXP synthase)
DXS OR RV2682C OR MT2736 OR MTCY05A6.03C
                                                                                                                                                                Indels
                                                                                            Length
                       95343 MW; 13BA634CCE7AA502 CRC64;
                                                                                                                                                             8
                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             638 AA
                                                                                                                                                          4; Mismatches
                                                                                                                              42;
                                                                                               Score 45.5;
                                                                                                                              Pred. No.
POLY-GLN
                                                                                                                                                                                                                                                                2 OHLKRVQL-RDVSEAEVROHREA 23
                                                                                            39.98;
                                                                                                                    Local Similarity 43.5%;
les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                           850 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1773;
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Gaps

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Indels

6; Mismatches

Conservative

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RESULT 14
NFM_CHICK
Matches
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                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-SCARC / AB972;

MEDLINE-94378003; PubMed-8091229;

MEDLINE-94378003; PubMed-8091229;

Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,

Johnston M., Andrews S., Brinkman R., Cooper J., Kirsten J.,

Rucaba T., Hillier L., Jier M., Johnston L., Langston Y.,

Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,

Nan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,

Night D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Saccharopta; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                  pfam; PF03779; transket_pyr; 1.
Pfam; PF03779; transket_lase_C; 1.
TigRPAMs; TigRANG0204; dxs; 1.
PROSITE; PS00801; TRANSKETOLASE_1; 1.
PROSITE; PS00802; TRANSKETOLASE_2; 1.
Transferase; Flavoprotein; Thiamine pyrophosphate;
Isoprene biosynthesis; Thiamine biosynthesis; Complete proteome.
SEQUENCE 638 AA; 67885 MW; 6F8DC2A78290873F CRC64;
                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Hypothetical 86.7 kDa protein in EGD2-SUN1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 763;
63;
                                                                                                                                                                                                                                                                                                                                  DB 1; Length 638; 37;
                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEOUENCE 763 AA; 86666 MW; 14A3AE9A21F11711 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          763 AA
                                                                                                                                                                                                                                                                                                                                                                         7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44;
Pred. No. 6
                                                                         TIGR; MT2756; -.
Tuberculist; Rv2682c; -.
HAMAP; MF 00315; -; 1.
InterPro; IPR005477; Dxs.
InterPro; IPR005475; Transketolase_C.
InterPro; IPR005475; Transketolase_CR.
InterPro; IPR005474; Transketolase_N.
                                                                                                                                                                                                                                                                                                                                         Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                        2 OHLKRVOLRDVSEAEVRO---HREA 23
                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U00030; AAB68356.1; -. PIR; S46678; S46678. S46079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.6%;
35.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                                            39.5%;
                                          , AE007105, AAK47071.1;
E70528, E70528.
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 44.0
Matches 11; Conservative
                            EMBL; Z96072; CAB09493.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YHZ7 YEAST
P38883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaudin M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THR197W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YHZ7_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
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Best Local Similarity

Query' Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THEORY OF THE PROTEINS: L, M, Genes Dev. 1:699-708(1987).

Genes Dev. 1:699-708(1987).

-I. FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M, Genes Dev. 1:699-708(1987).

-I. FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M, HICH ARE INVOLVED IN THE MAINTENER R.S. P. NEW IS PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THE FORMATION OF THOUGHT THAT PHOSPHORYLATION OF NPH RESULTS IN THE FORMATION OF THOUGHT THAT PHOSPHORYLATION OF NPH RESULTS IN THE FORMATION OF NPH RESULTS IN THE FORMATION OF THOUGHT THAT PROSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H). THE CONTRIBUTION COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.

- I. SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-88112814; PubMed-3123320;
Zopf D., Hermans-Borgmey'er I., Gundelfinger E.D., Betz H.;
Indentification of gene products expressed in the developing chick
visual system: characterization of a middle-molecular-weight
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=90174973; PubMed=2106668;
ADDLINE=90174973; PubMed=2106668;
Zopf D., Dineva B., Betz H., Gundelfinger E.D.;
"Isolation of the chicken middle-molecular weight neurofilament (NF-M) gene and characterization of its promoter.";
NP-M) gene and characterization of its promoter.";
Nucleic Acids Res. 18:521-529(1990).
                                                                                                                                                                                                                  01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neurofilament triplet M protein (160 kDa neurofilament protein)
(Neurofilament medium polypeptide) (NP-M).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Neurone; Phosphorylation;
                                                                                                                                                                 857 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X05558; CAA29073.1; -.
PIR; S15762; S15762.
INTERPRO; IPR006821; Fllament_head.
InterPro; IPR001664; IF.
InterPro; IPR0015957; Keratin_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00038; filament; 1.
Pfam; PF04732; filament head; 1.
PRINTS; PR01248; TYPEIKERATIN.
                                                        3 HLKRVQLRDVSEAEVROHRE 22
                                                                                                                                                                                                            01-APR-1990 (Rel. 14, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X17102; CAA34958.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 259-857 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAA29073.1;
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98
406
                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein.
INIT_MET
7.
                                                                                                                                                                           NFM CHICK
                                                                                                                                                                                                                                                                                                                                                                                              Gallus
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                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN: COMPOSED OF THREE STRUCTURAL DOMAINS: A LARGE GLOBULAR N-TERMINAL DOWAIN WHICH IS RESPONSIBLE FOR THE MOTOR ACTIVITY OF KINESIN (IT HYDROLYZES ATP AND BINDS MICROTUBLLE), A CENTRAL ALPHA-HELICAL COILLED COIL DOWAIN THAT MEDIATES THE HEAVY CHAIN DIMERIZATION; AND A SMALL GLOBULAR C-TERMINAL DOMAIN WHICH INTERACTS WITH OFFER REOTEINS (SUCH AS THE KINESIN LIGHT CHAINS),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 355-585 FROM N.A.
Engelender S., Sharp A.H., Colomer V., Tokito M.K., Lanahan A.,
Worley P., Holzbaur E.L.F., Ross C.A.;
Worley P., Holzbaur E.L.F., Ross C.A.;
"Huntingtin associated protein I (HAPI) interacts with the p150Glued
subunit of dynactin.";
Submitted (UNI-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: KINESIN IS A MICROTUBULE-ASSOCIATED FRORE-PRODUCING
PROTEIN THAT MAY PLAY A ROLE IN ORGANELLE TRANSPORT.
-!- SUBUNIT: OLIGOMER COMPOSED OF TWO HEAVY CHAINS AND TWO LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Kinesin heavy chain isoform 5C (Kinesin heavy chain neuron-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA Res. 5:31-39(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BRAIN, PROSTATE, AND TESTIS, AND MODERATE EXPRESSION IN KIDNEY, SMALL INTESTINE, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VESICLES AND MEMBRANOUS ORGANELLES.
SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                      ö
                                                                                                                                   (BY SIMILARITY)
(BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
Nomura N., Ohara O.,
                                                                                                                                                                                                                  Score 44; DB 1; Length 857;
Pred. No. 72;
                                                                                                                                                                -> R (IN REF. 2).
4E2E0FC6AC64778B CRC64;
                                                                                                               COIL 2B.
O-LINKED (GLCNAC)
O-LINKED (GLCNAC)
                                                                                                                                                                                                                                                                                                                                                                                                    957 AA
                                                                                                                                                                                                                                                 4; Mismatches
                                                 COIL 1B.
LINKER 12.
                                                                                COIL 2A.
LINKER 2.
   TAIL.
COIL 1A.
                                   LINKER 1.
                                                                                                                                                                                                                                                                                                 1 ROHLKRVQLRDVSEAEVRQHREA 23
                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
MEDLINE=98290545; PubMed=9628581;
                                                                                                                                                                                  ММ.
                                                                                                                                                                                                             Query Match
Best Local Similarity 43.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIF5C OR NKHC2 OR KIAA0531
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                                                                                                                                                               546
857 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                             KF5C HUMAN
O60282; O95079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAINS
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                                                                                                                                                                CONFLICT
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.
                                                                                                                              MIM; 604593; -.
GO; GO:0005871; C:kinesin complex; TAS.
GO; GO:0005871; F:microtubule motor activity; TAS.
GO; GO:000596; P:organile organization and biogenesis; TAS.
InterPro; IPR001752; kinesin_motor.
PFam; PF00225; kinesin; 1,
PRINTS; PR00125; kinesin; 1,
PROSITE; PS00412; KINESINHEAVY.
PROSITE; PS0041; KINESIN MOTOR DOMAINI; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAINI; 1.
                                                                                                                                                                                                                                                                             MOCOT protein; Microtubules; ATP-binding; Coiled coil.
DOMAIN 1386 KINESIN-MOTOR (BY SIMILARITY).
DOMAIN 406 923 COILED COIL.
DOMAIN 859 956 GLOBULAR.
                                                                                                                                                                                                                                                                                                                                      MICROTUBULE-BINDING.

ATP (BY SIMILARITY).

TLKNVI -> STHASV (IN REF. 2)

S85 EFT -> DRV (IN REF. 2).

109494 MW; A9F25BBIC994122A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 81:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44;
                                                                        EMBL; AB011103; BAA25457.1; -. EMBL; AF010146; AAD01436.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                              38.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               33.3%;
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                                                                                                    HSSP; P56536; 2KIN.
Genew, HGNC:6325; KIF5C.
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174
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957 AA;
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Search completed: November 12, 2003, 19:48:00 Job time : 4.77358 secs

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1 RQHLKRVQ----LRDVSEAEVRQHREA 23

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O994g6 homo sapien Q8wpk0 oikopleura Q8mi06 neurospoleura Q92sw4 rhizobium m Q9vsi2 drosophila Q8wyp5 homo sapien Q8iza4 homo sapien Q8iza4 homo sapien Q8vyp6 neuseria sp Q9yuq1 neisseria m

O33230 mycobacteri O89je2 mycobacteri O89je2 mycobacteri O89ye34 pseudomonas Q8ekv1 oceanobacil O9v718 drosophila O4617 drosophila O9mky drosophila O9m6y9 drosophila O9m8f5 trypanosoma O9d632 xenopus lae O90814 drosophila O2604 homarus ame

Q8r3f9 mus musculu Q9wv65 rattus norv Q9kps6 vibrio chol Q9h5f4 homo sapien O8pxe5 methanosarc

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
ABG-deleted variant of telomerase reverse transcriptase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     807 AA.
             QBAV90
Q9Y4Q6
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Q9SW4
Q9SW4
Q9UZA4
QBIZA4
QBIZA4
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QBIZA4
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QBYZE2
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Q9KNP7
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PRELIMINARY;
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Best Local Similarity
Matches 21; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
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28NG38
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Q8HGG4 homo sapien
Q9r0b3 mus musculu
Q9rb3 rattus norv
Q9qxz4 mesocricetu
Q9gyd4 rhizobium 1
Q8x7n3 escherichia
Q8x7n3 escherichia
Q8yq2 leishmania
Q8yq2 leishmania
Q8yq4 1 leishmania
Q8upq4 agrobacteri
Q8bg9 acenorhabdi
Q8mu8 macaca
Q8mu8 macaca
Q8mu8 macaca fasc
Q8mu8 macaca
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                                                                                                     November 12, 2003, 19:42:29; Search time 21.9874 Seconds (without alignments) 269.937 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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1 ROHLKRVQLRDVSEAEVROHREA 23
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Maximum Match 100%
Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
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Q8N6C3
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Q9R0B3
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Q8WNU8
Q9VPL5
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sp_human:*
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seq length: 200000000
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Match Length DB
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807
1069
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Gaps

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Result 8

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Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                     Drissi R., Cleveland J.L.; signification of a mus musculus telomerase catalytic subunit intron."; "Sequence of a Mus musculus telomerase catalytic subunitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 0.004;
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Pred. No. 0.00035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wong S., Gao S., Xu X., Yu H.;
"Rat telomerase catalytic subunit, rTERT.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP247818; AAF62177.1;
InterPro; IPR000477; RVTSe.
InterPro; IPR003545; Telomerase_RT.
                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
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01-WAY-2000 (TYEMBLrel. 13, Last sequence update)
01-OCT-2002 (TYEMBLrel. 22, Last annotation update)
01-OCT-2002 (TYEMBLrel. 22, Last annotation update)
Telomerase catalytic subunit.
Wesocricetus auratus (Golden hamster)
                                                                                                                                                                                                                                                                                                      52 AA; 6479 MW; 41473425E44BDA9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1128 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ROHLKRVQLRDVSEAEVROHRE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 RQHLERVRLRELSQEEVRHHQD 45
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PRINTS; PR01365; TELOMERASERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.8%;
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59.1%;
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                                                                                                                                                                                                                                    EMBL; AF090439; AAD54013.1;
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Best Local Similarity 59.19
warches 13; Conservative
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Matches 13; Conservative
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Mus musculus (Mouse)
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                                                                                                                                  SEQUENCE FROM N.A.
                                                                     NCBI_TaxID=10090;
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SEQUENCE
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09лк99;
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Q9QXZ4
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Q9JK99
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Hisatomi H., Nagao K., Kanamaru T., Sumida H., Hirata H., Yamamoto M.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                               Kazumasa H.;
"Both beta and gamma deletion isoform of human telomerase reverse
"Both beta and gamma deletion isoform of human telomerase reverse
"Both beta and gamma deletion isoform of human telomerase.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB086379; BAC11014-1;
ThiterPro.; PRO1365; Telomerase_RT.
InterPro.; PRO1365; Telomerase_RT.
SEQUENCE 807 AA; 90225 MW; 199664460CE6D763 CRC64;
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1011_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 807;
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Hisatomi H., Nagao K., Hirata H., Hikiji K., Kanamaru T.,
Hisatomi H., Nagao K., Hirata H., Hikiji K., Kanamaru T.,
"Exon 11 deleted variant of the human telomerase reverse
transcriptase.";
Submitted (NAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB085628; BAC11010.1;
InterPro; IPR003545; Telomerase.RT.
InterPro; IPR003545; Telomerase.RT.
RNA-directed DNA polymerase.
ENDA-directed DNA polymerase.
SRQUENCE 1069 AA; 120047 MW; BELE77A653BIC666 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Beta and gamma deletion isoform of telomerase reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Best Local Similarity 91.3%; Pred. No. 7.2e-08;
Matches 21; Conservative 2; Mismatches 0.
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Matches 21; Conservative
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                                                                                                                                                              Homo sapiens (Human).
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Q9R0B3;
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Matches
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MEDLINE=21240330; Pubmed=11342218;
Guo W., Okamoto M., Lee Y.M., Baluda M.A.; Park N.H.;
"Enhanced activity of cloned hamster TERT gene promoter in transformed
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MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watenabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the nitrogen-fixing symbiotic bacterium
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Phyllobacteriaceae; Mesorhizobium.
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RNA-directed DNA polymerase; Transferase.
SEQUENCE 1128 AA; 128394 MW; 1D4F81249012174E CRC64;
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(TrEMBLrel. 22, Last annotation update)
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Last sequence update)
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55.0%; Pred. No. 12;
iive 3; Mismatches 6;
                                                                             Biochim. Biophys. Acta 1517:398-409(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               356 AA
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584 RHHLERVRLQELSQEEVRORGEA 606
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EMBL; AP002998; BAB49051.1; -.
InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR005467; His kināse.
InterPro; IPR00014; PAS domain.
Pf02518; HATPase_c; I.
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                                                                                            EMBL, AF149012; AAF1733.1;
InterPro; IPR000477; RVTse.
InterPro; IPR003545; Telomerase_RT.
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RQHLKDAHQRVLSVAEVQRH 204
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SMART; SM00091; PAS; 1.
PROSITE; PS50109; HIS_KIN; 1.
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es 13; Conserv
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01-MAR-2002 (
01-MAR-2002 (
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AC Q8
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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sequencing and
                                                                                                                                                                                                                                                                                                         STRAIN-0157:H7 (EDL933 / ATCC 700927;

MEDLINE-21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
"Genome sequence of entervhaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533 (2001).
                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
EMBL; AE05202; AAG54569.1;
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
NCBI_TaxID=55884;
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MEDLINE=97449297; PubMed=9305766;
MEDLINE=97449297; PubMed=9305766;
Midline=97449297; PubMed=9305766;
Midline=10., Mastin D.A., Lindberg A.A., Verma N.K.
Shiqella flexneri type-specific antigen V: cloning, sequencing
characterization of the glucosyl transferase gene of temperate
bacteriophage SfV.";
Gene 195:207-216(1997).
EMBL: U82619; AAB72135.1; -
HSSP; P21442; IAIH.
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Pfam; PF00589; Phage integrase; 1.
SEQUENCE 387 AA; 44839 MW; EC245FAAC8007690 CRC64;
01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Putative integrase for prophage CP-933H.
INTH OR EC3037 OR ECS027!.
Escherichia coli 0157:H7.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
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7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 QHLKRVQLRDVSEAEV-----RQHRE 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP002551; BAB33694.1; -.
InterPro; IPR002104; Phage_integrase.
Pfam; PF00589; Phage_integrase; 1.
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STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
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1584 AA; 168226 MW; AB2A79A3B4E28E07 CRC64;
                                                                                                         1381 КЕНККІГНОКОТООАОVAO 1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e; Complete proteome.
221 AA; 24333 MW;
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38.9%;
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Genome Res. 8:135-145(1998).
EMBL; AL359716; CAD19413.1;
Transmembrane.
SEQUENCE 1584 AA; 168226
                                                   43.0%;
                                                             47.48;
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Matches 7; Conservative
                                           ransferase;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical predicted helix-turn-helix transmembrane protein P265.04,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                    Gaps
                                                                                                                                                                              Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
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Robben J., Grymonprez B., Weltjens I., Aert R., Volckaert G.,
Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98146435; PubMed=9477341;
Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
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                                                                                                                                                                                                                                                                                                     STRAIN=Friedlin;
MEDLINE=98146435; PubMed=9477341;
Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Santh D.F.;
                                                                                                                                                                                                                                                                                                                                                                                               DB 5; Length 1268;
                                                                                                                                                                                                                                                                                                                                  "A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
EMBL; AL391629; CAC05311.1;
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEOUENCE 1268 AA; 135809 MW; C65F35A2164CB040 CRC64;
                                                                                                                                                                                                                                           Oliver K., Murphy L., Harris D., Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                     Indels
                                                                                                                                        01-WAR-2001 (TrEMBLrel. 16, Last sequence update) 01-WAR-2001 (TrEMBLrel. 16, Last annotation update) Hypothetical 135.8 kba protein.
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4; Mismatches
                                                         Pred. No. 22;
7; Mismatches
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1065 REHKKRLHQRDTQDAQVAQ 1083
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               33.3%;
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                                          2 QHLKRVQLRDVSEAEV-
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                          10, Conservative
                                                                                                                   PRELIMINARY;
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les 9, Conserv
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Matches 10, Conserv
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Matches
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MEDLINE=21608551; PubMed=11743194; Miller N., Blanchard M.,

Goodner B., Hinkle G., Gattung S., Miller N., Halling C., Mullin L.,

Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,

Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,

Houmiel K., Gordon J., Vaudin W., Scott C., Lappas C., Markelz B.,

Wollam C., Allinger M., Doughty D., Lomo C., Sear C., Strub G.,

Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,

Cielo C., Slater S.,
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                                                               Gaps
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Science 294:2323-2328(2001).
EMBL; AE009228; AAL43788.1; ALT_INIT.
EMBL; AE008194; AAK88520.1;
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                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Cob(I) alamin adenosyltransferase.
COBO OR ATUZ807 OR AGR C_5090.
Agrobacterium tumefaciens (strain CS8 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium.
NTBI_TaxID=176299;
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                                                                     6; Indels
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29;
Score 49; DB 5; I
Pred. No. 1.1e+02;
4; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                221 AA
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Pred. No. 2
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InterPro; IPR000299; Band 4.1.

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Hypothetical protein; Complete proteome.

SEQUENCE 270 AA; 31019 MW; AASA4C8E94FBIEFE CRC64;
                                                                                                                       Pyrococcus horikoshii.
Archaea, Euryarchaeota, Thermococci, Thermococcales, Thermococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.2%; Score 47; DB 17; Length 270; 37.0%; Pred. No. 36; .ive 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Bristol N2;
Favello A., FavelloA;
"The sequence of C. elegans cosmid T04C9.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U80955; AAG01559.2; -.
WormPep; T04C9.6; CE29463.
                   01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Pypothetical protein PH1189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MRR-2001 (TrEMBLrel. 16, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 65.7 kDa protein.
                 270 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           573 AA
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152 KHLKEAKAQDISELQVQINNLTRENRE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 OHLKRVQLRDVSEAEV-----RQHRE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                              MEDLINE=98344137; PubMed=9679194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Conservative
                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waterston R.;
"Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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STRAIN=Bristol N2;
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                                                                                                                                                                  NCBI_TaxID=53953;
                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T04C9.6
                 058907
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Q9GP93
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-1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

REMBL: AB064997; BAB83539.1;

INTERFYO; IPR000199; PROT kinase.

RILEFPRO: IPR001295; Tyr_Dkinase.

RILEFPRO: IPR001290; Tyr_Dkinase.

REMIN: PR00069; Pkinase; I.

REMIN: PR000609; Pkinase; I.

REMIN: PR000019; Prot_kinase; I.

REMIN: PR00011; Prot_kinase; I.

REMOSTE: PS001019; PROTEIN KINASE DOW; I.

REMOSTE: PS001019; PROTEIN KINASE ST; I.

REMOSTE: PS001019; PROTEIN KINASE ST; I.

REMOSTE: PS001019; PROTEIN—KINASE ST; I.
                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Testis;
Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,
Terao K., Suzuki Y., Sugano S.;
"Isolation of novel full-length cDNA clones from macaque testis
                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
mRNA, similar to human hypothetical protein FLJ23495, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                    41.2%; Score 47; DB 5; Length 573; 42.1%; Pred. No. 78;
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                                                                                                                                                                                              7; Indels
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                                                                                    Hypothetical protein. — -
SEQUENCE 173 Aa; 65747 MW; A45FE0A562AE05ED CRC64;
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9
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45.0%; Pred. No. 86;
ive 6; Mismatches
                                                                                                                                                                                              4; Mismatches
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Job time : 22.1541 secs
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PERNTS; PRO0935; BAND41; 1. PRINTS; PRO0935; BAND41. PROSITE; PS00660; BAND 41 1; 1. PROSITE; PS50057; BAND 41 3; 1.
                                                                                                                                                                                                                                      1 RQHLKRVQLRDVSEAEVRQ 19
                                                                                                                                                                                            8; Conservative
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                                                                                                                                                                  Local Similarity
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Best Local Similarity
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Matches
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Human telomerase p Altered C-terminus Altered C-terminus Altered C-terminus Altered C-terminus Telomerase protein Telomerase (ver. 2 Human telomerase c Human telomerase r Human telomerase r

Truncated telomera Truncated telomera N-terminal truncat Truncated telomera

Glutathione-S-tran A catalytic telome Human CRT-1 protei Amino acid sequenc

Human telomerase r N-terminal truncat Truncated telomera A human telomerase Human telomerase r Human telomerase r Human EST2 protein Human telomerase r Human telomerase p Truncated telomera

Human catalytic te hEST2, a human tel Human telomerase r Human telomerase p

Heart muscle cell

Scoring table:

Searched:

Database

score:

Perfect

Sequence:

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protein

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Run on:

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Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis;
prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
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                                                   AAW97384
AAY25463
AAW46997
AAY00637
AAY00646
AAY00642
AAY00653
             ABB99679
ABB99678
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AAY00640
AAY00649
AAY00641
AAY00650
AAW1376
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AAY43621
AAY32090
AAY28401
AAY26580
AAY00627
AAY00638
AAW90221
AAW90221
AAW90221
AAW90221
AAW90221
AAW90566
AAB92765
AAB92765
AAB93930
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96US-0724643.
97US-0844419.
97US-0851843.
97US-0851843.
97US-081312.
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14-AUG-1997;
14-AUG-1997;
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18-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
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 Human telomerase r
Human telomerase r
Splice variant of
Amino acid sequenc
Splice variant of
Human telomerase r
Human telomerase r
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Human CRT-1 protei
                                                                                November 12, 2003, 19:41:04 ; Search time 33.6226 Seconds (without alignments) 127.462 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                      A Geneseq 19Jun03:*

| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
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                                                                                                                                                                                                                                                          1107863
      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                           1 ARTFRREKRAERLTSRVKALFSVLNYE 27
                                                                                                                                                                                                                               1107863 segs, 158726573 residues
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                                                         protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                  Listing first 45 summaries
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AAW57389
ABB99682
AAW97385
ABB99681
AAY43128
AAY43128
AAY4461
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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27
108
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130 130 130 130 130

2 m 4 m 6 L 80 0

Score

Result

(UYTE-) UNIV TECHNOLOGY CORP.

Lingner J;

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The present sequence represents an antigenic peptide from human ct elementase reverse transcriptase (HTRT), from the present invention. The present invention also describes the following methods: (A) determining present invention also describes the following methods: (A) determining compensation of protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a compound; (B) preparation of recombinant telomerase by contacting a compound; (B) preparation of from a telomerase RNA component; (C) protein preparation of hTRT with a telomerase RNA component; (C) protein of the hTRT RNA or protein in a sample by binding a relevant detection, amplifying the product and correlating the presence of RNA detection, amplification product and correlating the presence of C and (D) increasing the proliferation of a vertebrate cell by increasing call vertebrate cell proliferation of a vertebrate cell by increase in the manufacture of medicament that inhibits cell vertebrate cell proliferation of hTRT and the polynucleotide encoding ageing. A protein preparation of hTRT and the polynucleotide encoding effect of ageing or cancer. Inhibitors of telomerase activity can be used in the manufacture of medicaments for inhibiting the manufacture of medicaments and the new machods.
                                                                                              Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis;
prognosis; cell proliferation; cancer; ageing; ribonucleoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human telomerase reverse transcriptase antigenic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 130; DB 19; Length
100.0%; Pred. No. 1e-12;
-tye 0; Mismatches 0; Indels
                      Harley C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAWS7389 standard; peptide; 27 AA.
                      Chapman KB,
Harley CB;
                                                                                                                                                                         Example 8; Fig 54; 387pp; English.
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96US-0724643.
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97US-0846017.
97US-0851843.
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Best Local Similarity luv...
Best Local 27; Conservative
                          , Cech TR,
Nakamura T,
                                                                            WPI; 1998-171633/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 AA;
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25-APR-1997;
06-MAY-1997;
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                                 Andrews WH,
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                                               Morin GB,
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The present sequence represents an autityeant preparate the invention. The telomerase reverse transcriptase (hTRT), from the present invention. The present invention also describes the following methods: (A) determining the change whether a test compound is a modulator of hTRT, by detecting the change compound; (B) preparation of recombinant telomerase by contacting a compound; (B) preparation of recombinant telomerase by contacting a compound; (B) preparation of probe to the sample and detecting the complex formed or in the case of probe to the sample and detecting the complex formed or in the sample; (C) probe to the sample and detecting the complex formed or in the sample; (C) may detection, amplifying the product and correlating the presence of probe to the sample and detecting the complex formed or in the sample; (C) and (D) increasing the product with presence of hTRT in the sample; (C) and (D) increasing the proliferation of a vertebrate cell by increasing the proliferation of cancer a medicament that inhibits collipse ageing. A protein preparation of hTRT and that inhibiting the hTRT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be effect of ageing or cancer. Inhibitors of telomerase activity, a protein preparation of hTRT can also be used in the new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Splice variant of a human telomerase reverse transcriptase fragment.
                                                                                                                                                                                              Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; telomerase reverse transcriptase; hTERT; T cell response;
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0
                                                                                                                                                                                                                                                                                                     The present sequence represents an antigenic peptide from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 130; DB 19; Length 27; 100.0%; Pred. No. 1e-12; 0; Indels 0 tive 0; Mismatches 0; Indels 0
                                                                                                              Lingner J;
                                                                                                                Harley C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ARTFRREKRAERLTSRVKALFSVLNYE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB99682 standard; protein; 108 AA.
                                                                                                                                                                                                                                                                            Example 8; Page 259; 387pp; English.
                                                                                                                    Chapman KB,
Harley CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAY-2001; 2001GB-0012342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MAY-2002; 2002WO-NO00176.
                                                                   (GERO-) GERON CORP.
(UYTE-) UNIV TECHNOLOGY CORP.
97US-0854050.
97US-0911312.
97US-0912951.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.
Best Local Similarity 100.
Matches 27; Conservative
                                                                                                                       , Cech TR,
Nakamura T,
                                                                                                                                                                          WPI; 1998-171633/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200294312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAR-2003
     09-MAY-1997;
                   14-AUG-1997;
14-AUG-1997;
                                                                                                                           Andrews WH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB99682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                         Morin GB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
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Gaps

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Indels

Length 131;

Score 130; DB 20; Pred. No. 5.8e-12;

0; Mismatches

ilarity 100.0%; Conservative 0

27;

100.0%;

131 AA;

27

101 ARTFRREKRAERLTSRVKALFSVLNYE 127

1 ARTFRREKRAERLTSRVKALFSVLNYE

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New polypeptides derived from human telomerase reverse transcriptase, useful in preparing a medicament for treating or preventing cancer, or in preparing a diagnostic for diagnosing cancer, e.g. breast cancer or
                                                                                                                                                                                                                                      Splice variant of a human telomerase reverse transcriptase fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 2; 56pp; English.
                                                                                                                                                                   ABB99681 standard; protein; 174
                                                                                                                                                                                                                                                                                                                                                                     16-MAY-2002; 2002WO-NO00176.
                                                                                                                                                                                                                                                                                                                                                                                          21-MAY-2001; 2001GB-0012342.
                                                                                                                                                                                                                 28-MAR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-129380/12.
                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 (GEMV-) GEMVAX AS
                                                                                                                                                                                                                                                                            vaccine, cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prostate cancer
                                                                                                                                                                                                                                                                                                                       WO200294312-A1
                                                                                                                                                                                                                                                                                                                                              28-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eriksen JA,
                                                                                                                                                                                           ABB99681;
                   Sequence
                                                                                                                                                                                                                                                                Human;
                                                              Matches
                                                                                                                                                          ABB9968
                                                                                                                                                                    원
                                                                                     ò
                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                               The present sequence represents a splice variant of a fragment of human telomerase reverse transcriptase (hTERT). The specification describes peptides derived from hTERT, which are capable of inducting a T cell response and are used in medicine. The hTERT peptides and nucleic acids encoding them are useful in preparing a medicament, which is a vaccine, an antisense molecule, or is capable of generating an antisense molecule in vivo, for treating cancer, or in preparing a diagnostic for diagnosing pancer. The cancer is, for example, breast cancer, prostate cancer, pancreatic cancer, colo-rectal cancer, lung cancer, malignant melanoma, leukemia, lymphoma, ovarian cancer, cervical cancer, or a biliary tract
                                                                   New polypeptides derived from human telomerase reverse transcriptase, useful in preparing a medicament for treating or preventing cancer, or in preparing a diagnostic for diagnosing cancer, e.g. breast cancer or prostate cancer
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Catalytic telomerase; diagnosis; disease; telomerase activity.
                                                                                                                                                                                                                                                                                                                     Length 108;
                                                                                                                                                                                                                                                                                                                                           Indels
                          Saeboe-Larssen S;
                                                                                                                                                                                                                                                                                                                    100.0%; Score 130; DB 24; 100.0%; Pred. No. 4.7e-12;
                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of the specification.
                                                                                                                                                                                                                                                                                                                                                               1 ARTFREKRAERLTSRVKALFSVLNYE 27
                                                                                                                                                                                                                                                                                                                                                                               Moller M,
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW97385 standard; Protein; 131 AA
                                                                                                                            Disclosure, Fig 2; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MITU ) MITSUBISHI CHEM CORP
                        Gaudernack G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97JP-0207708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
es 27; Conservative
                                             WPI; 2003-129380/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-208111/18.
N-PSDB; AAX15924.
                                                                                                                                                                                                                                                                                          108 AA;
 (GEMV-) GEMVAX AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP11046768-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1997;
                      Eriksen JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAY-1999
                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW97385;
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telomerase reverse transcriptase; hTERT; T cell response;

Gaudernack G, Moller M, Saeboe-Larssen S;

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The present sequence represents a splice variant of a fragment of human telomerase reverse transcriptase (hTERT). The specification describes peptides derived from hTERT, which are capable of inducing a T cell response and are used in medicine. The hTERT peptides and nucleic acids encoding them are used in medicine. The hTERT peptides and nucleic acids an antisense molecule, or is capable of generating an antisense molecule in vivo, for treating cancer, or in preparing a diagnostic for diagnosing cancer. The cancer is, for example, breast cancer, prostate cancer, pancreatic cancer, colo-rectal cancer, lung cancer, malignant melanoma, leukemia, lymphoma, ovarian cancer, cervical cancer, or a biliary tract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 130; DB 24; 100.0%; Pred. No. 7.9e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
100.0%; Constitute 100.0%; Pred. No. 7.9
Matches 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 ARTFRREKRAERLTSRVKALFSVLNYE 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ARTFRREKRAERLTSRVKALFSVLNYE 27
                                                                                                                                                                                                                                                                                                                                                                                                                             174 AA;
                                                                                                                                                                                                                                                                                                                                                         carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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RESULT 6

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New catalytic protein of telomerase of a higher animal and a gene coding it - useful for diagnosis of diseases caused by the change activity of a telomerase

coding

Example 1; Page 14; 18pp; Japanese.

The specification describes a human catalytic telomerase protein. The products are useful in drug compositions for the diagnosis of diseases caused by the change in activity of telomerase. The present sequence appears in the specification.

AAY43128 standard; Protein; 283 AA.

20-DEC-1999

AAY43128;

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RESULT 7
AAY43128
                                                           The present sequence represents a human telomerase reverse transcriptase (ThTR) protein from a cDNA clone from the present invention. The present invention also describes the following methods: (A) determining whether invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polynucleotide, on administration of the compound; (C) detecting of recombinant telomerase NAA component; (C) detection of preparation of hTRT with a telomerase RNA component; (C) detection of preparation of hTRT with a telomerase RNA component; (C) detection of cample and detecting the complex formed or in the case of RNA detection, camplifying the product and correlating the presence of fTRT in the sample; and (D) amplification product with presence of hTRT in the sample; and (D) amplification product with presence of hTRT in the sample; and (D) complification product with presence of hTRT in the sample; and (D) amplification product with presence of hTRT and that causes in cell correspond; and (B) the use of an agent that causes an increase in cell corresponding of hTRT and the polynucleotide encoding ageing. A protein preparation of hTRT and the polynucleotide encoding contract of ageing or cancer. Inhibitors of telomerase activity can be effect of ageing or cancer. Inhibitors of telomerase activity can be activity. A protein preparation of hTRT can also be used in the new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                         Human telomerase reverse transcriptase protein from cDNA clone 712562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                 Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis;
prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 259;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harley C, Lingner J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 130; DB 19;
100.0%; Pred. No. 1.2e-11;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chapman KB,
Harley CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 19; 387pp; English
AAW46998 standard; Protein; 259 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GERO-) GERON CORP.
(UYTE-) UNIV TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                      97US-0915503.
96US-0724643.
97US-0844419.
97US-0851843.
97US-0851843.
97US-0851813.
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                                                                                                                                                                                                                                                                                                                                                  97GB-0020890
                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cech TR,
Nakamura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-171633/16.
N-PSDB; AAV22379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 AA;
                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                      01-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΜH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-MAY-1997
14-AUG-1997
                                                                                                                                                                                                                                                                        GB2317891-A
                                                                                                                                                                                                                                                                                                              08-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                      18-APR-1997
25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAY-1997
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                                                                                    13-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Morin GB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andrews
                                              AAW46998;
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Conservative

Matches

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This sequence represents the human telomerase reverse transcriptase (hTERT). The invention relates to a monoclonal antibody recognising the hTERT. The antibody can be used for the investigation, diagnosis and treatment of telomerase-related diseases, especially diseases in which telomerase expression is up-regulated e.g. cancers.
                                                                                                                                                                                                                                                                                                                     telomerase catalytic subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Splice variant of a human telomerase reverse transcriptase fragment.
                                                                                                                                                                                                                                                            Ξ
                     reverse transcriptase; hTERT; antibody; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; telomerase reverse transcriptase; hTERT; T cell response;
                                                                                                                                                                                                                                                              Anazawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                              Mikuni O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 130; DB 20;
100.0%; Pred. No. 1.4e-11;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                        New monoclonal antibody recognizing human telomera (hTERT) useful for treating and diagnosing cancer
                                                                                                                                                                                                                                                               Furuya A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ARTFREKRAERLTSRVKALFSVLNYE 27
Human telomerase reverse transcriptase.
                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 72-73; 78pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB99680 standard; protein; 436 AA.
                                 Human telomerase reverse transcript
telomerase-related disease; cancer
                                                                                                                                                                                                                                                                 Yamasaki M, Shibata K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAY-2002; 2002WO-NO00176.
                                                                                                                                                                                                                                    (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                       98JP-0098486.
                                                                                                                                                                         99WO-JP01557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.'
Marches 27; Conservative
                                                                                                                                                                                                                                                                                                   WPI; 1999-591316/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200294312-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-NOV-2002
                                                                                                               WO9950407-A1.
                                                                                  Homo sapiens.
                                                                                                                                                                             26-MAR-1999;
                                                                                                                                                                                                        26-MAR-1998;
                                                                                                                                                07-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB99680;
                                                                                                                                                                                                                                                                       Hanai N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB99680
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Gaps

us-08-854-050-114.rag

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This invention describes novel human CRT-1 genes and their encoded proteins containing a reverse transcriptase motif, which act as telomerase inhibitors. The gene, its encoded protein and derived antibodies can be used to provide base sequence information, detect telomerase activity and cancer cells, and to screen telomerase inhibitors. The detection method is simple and effective.
                                                 Novel gene, useful in detection of telomerase activity and cancer cells as well as screening telomerase inhibitors for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel gene, useful in detection of telomerase activity and cancer cells as well as screening telomerase inhibitors for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel human CRT-1 genes and their encode proteins containing a reverse transcriptase motif, which act as telomerase inhibitors. The gene, its encoded protein and derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRT-1; reverse transcriptase; telomerase; inhibitor; detection; telomerase activity; cancer cell; screening; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stop codon given"
                                                                                                                                                                                                                                                                                                                      Length 437;
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                        DB 20;
                                                                                                                                                                                                                                                                                                                  100.0%; Score 130; DB 20;
100.0%; Pred. No. 2.2e-11;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= CRT-1
/note= "Partial sequence, no
                                                                                                                                                                                                                                                                                                                                                                                                              1 ARTFREKRAERLTSRVKALFSVLNYE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 35-36; 44pp; Japanese.
                                                                                                                        Claim 2; Page 31-32; 44pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY25462 standard; Protein; 438 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-JP00039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yoshida K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human CRT-1 protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..438
WPI; 1999-430393/36.
N-PSDB; AAX88243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-430393/36.
                                                                                                                                                                                                                                                                                 437 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAX88250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JAN-1998;
30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rsuchiya M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY25462;
                                                                                                                                                                                                                                                                                    Sequence
                                                                                        cancers
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                                                                                                                                                                                                                                                                        The present sequence represents a splice variant of a fragment of human telomerase reverse transcriptase (hTERT). The specification describes peptides derived from hTERT, which are capable of inducing a T cell response and are used in medicine. The hTERT peptides and nucleic acids encoding them are used in medicine. The present, which is a vaccine, an antisense molecule, or is capable of generating an antisense molecule in vivo, for treating cancer, or in preparing a diagnostic for diagnosing cancer. The cancer is, for example, breast cancer, prostate cancer, pancreatic cancer, colo-rectal cancer, lung cancer, malignant melanoma, leukenia, lymphoma, ovarian cancer, cervical cancer, or a biliary tract
                                                                                                                                          New polypeptides derived from human telomerase reverse transcriptase, useful in preparing a medicament for treating or preventing cancer, or in preparing a diagnostic for diagnosing cancer, e.g. breast cancer or prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRT-1; reverse transcriptase; telomerase; inhibitor; detection; telomerase activity; cancer cell; screening; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                   Saeboe-Larssen S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 130; DB 24;
100.0%; Pred, No. 2.2e-11; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ARTFRREKRAERLTSRVKALFSVLNYE 27
                                                                                 Moller M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY25461 standard; Protein; 437 AA
                                                                                                                                                                                                                                          Disclosure; Fig 2; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ...437
'label= CRT-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98JP-0139177.
98JP-0013232.
98JP-0033584.
           21-MAY-2001; 2001GB-0012342
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                                                                                 Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27; Conservative
                                                                                 Eriksen JA, Gaudernack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tsuchiya M, Yoshida K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human CRT-1 protein #1
                                                                                                                  WPI; 2003-129380/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              436 AA;
                                          (GEMV-) GEMVAX AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-MAY-1998;
08-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9935261-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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The present sequence represents a fragment of human telomerase reverse transcriptase (hTERT). The specification describes peptides derived from hTERT, which are capable of inducing a T cell response and are used in medicine. The hTERT peptides and nucleic acids encoding them are useful in preparing a medicament, which is a vaccine, an antisense molecule, or is capable of generating an antisense molecule in vivo, for treating cancer, or in preparing a diagnostic for diagnosing cancer. The cancer is, for example, breast cancer, prostate cancer, pancreatic cancer, colo-rectal cancer, unique cancer, malignant melanoma, leukemia, lymphoma, ovarian cancer, cervical cancer, or a biliary tract carcinoma.
                                                                                                                                                                                      Amino acid sequence of human telomerase reverse transcriptase fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptides derived from human telomerase reverse transcriptase, useful in preparing a medicament for treating or preventing cancer, or in preparing a diagnostic for diagnosing cancer, e.g. breast cancer or prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
                                                                                                                                                                                                                                Human; telomerase reverse transcriptase; hTERT; T cell response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glutathione-S-transferase and hTRT fusion protein 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 130; DB 24; 100.0%; Pred. No. 2.5e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ARTFREEKRAERLTSRVKALFSVLNYE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARTFRREKRAERLTSRVKALFSVLNYE 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moller M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW47002 standard; Protein; 531 AA
                                                             ABB99678 standard; protein; 499 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 2, 56pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAY-2002; 2002WO-NO00176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAY-2001; 2001GB-0012342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaudernack G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-129380/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            499 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEMV-) GEMVAX AS
                                                                                                                                                                                                                                                          vaccine; cancer.
                                                                                                                                                                                                                                                                                                                                            WO200294312-A1.
                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                 28-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eriksen JA,
                                                                                                                                                                                                                                                                                                                                                                                    28-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW47002;
                                                                                                         ABB99678;
                   RESULT 12
                                              4BB9967
                                                                                     g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptides derived from human telomerase reverse transcriptase, useful in preparing a medicament for treating or preventing cancer, or in preparing a diagnostic for diagnosing cancer, e.g. breast cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Splice variant of a human telomerase reverse transcriptase fragment.
antibodies can be used to provide base sequence information, detect telomerase activity and cancer cells, and to screen telomerase inhibitors. The detection method is simple and effective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; telomerase reverse transcriptase; hTERT; T cell response;
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                                                                                                                             Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 130; DB 24;
100.0%; Pred. No. 2.3e-11;
iive 0; Mismatches 0;
                                                                                                                               100.0%; Score 130; DB 20;
100.0%; Pred. No. 2.2e-11;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                         1 ARTFREEKRAERLTSRVKALFSVLNYE 27
                                                                                                                                                                                                                 1 ARTFRREKRAERLTSRVKALFSVLNYE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moller M,
                                                                                                                                                                                                                                                                                                                                                                    ABB99679 standard; protein; 463 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAY-2002; 2002WO-NO00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAY-2001; 2001GB-0012342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaudernack G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-MAR-2003 (first entry)
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Matches 27; Conservative
                                                                                                                                                                         27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-129380/12.
                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463 AA;
                                                                                     438 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEMV-) GEMVAX AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccine; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200294312-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                          Sequence
                                                                                                                                    Query Match
                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                          RESULT 11
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Saeboe-Larssen

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Gaps

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Length 499; Indels

Region Region

us-08-854-050-114.rag

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New catalytic protein of telomerase of a higher animal and a gene coding it - useful for diagnosis of diseases caused by the change in activity of a telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a catalytic telomerase protein. The products are useful in drug compositions for the diagnosis of diseases caused by the change in activity of telomerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRT-1; reverse transcriptase; telomerase; inhibitor; detection; telomerase activity; cancer cell; screening; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Partial sequence, no stop codon given"
                                                                                                                                                                                                             Catalytic telomerase; diagnosis; disease; telomerase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 100.0%; Score 130; DB 20; Local Similarity 100.0%; Pred. No. 3.1e-11; es 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 ARTFRREKRAERLTSRVKALFSVLNYE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ARTFRREKRAERLTSRVKALFSVLNYE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 11-14; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY25463 standard; Protein; 622 AA
                                                                                                                                                   A catalytic telomerase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..622
/label= CRT-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MITU ) MITSUBISHI CHEM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97JP-0207708.
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98JP-0013232.
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                                                                                         14-MAY-1999 (first entry)
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N-PSDB; AAX15923.
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                                                                                                                                                                                                                                                                                                                               JP11046768-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9935261-A1.
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08-JAN-1998;
                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                            23-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a fusion protein from an example of the present invention which describes human telomerase reverse transcriptase (hTRT). The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polynucleotide, on administration of the compound;

(B) preparation of recombinant telomerase by contacting a protein preparation of hTRT with a telomerase by component; (C) detection of the hTRT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of HTRT in the sample; and (D) increasing the product with presence of HTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTRT expression; and (E) the use of an agent that causes an increase in cell vertebrate cell proliferation of reate a medicament that inhibits ageing. A protein preparation of hTRT and the polynucleotide encoding hTRT can be used in the manufacture of medicaments for inhibiting the used to treat conditions that are associated with high telomerase contactions that are associated with high telomerase
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                                                                                     1..21
/note= "glutathione-S-transferase fragment"
249..531
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Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 27; Conservative 0; Mismatches 0;
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                                                                                                                                                                        /note= "hTRT protein fragment"
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                                                       Location/Qualifiers
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Harley CB;
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96US-0724643.
97US-0844419.
97US-0846017.
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Nakamura T,
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01-OCT-1996;
18-APR-1997;
25-APR-1997;
06-MAY-1997;
Homo sapiens
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14-AUG-1997,
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                                                                                                                                                                                                                                                                                             08-APR-1998
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Sequence

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Length 591; Indels

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This invention describes novel human CRT-1 genes and their encoded proteins containing a reverse transcriptase motif, which act as telomerase inhibitors. The gene, its encoded protein and derived antibodies can be used to provide base sequence information, detect telomerase activity and cancer cells, and to screen telomerase inhibitors. The detection method is simple and effective.
                                                                                                                                                   Novel gene, useful in detection of telomerase activity and cancer cells as well as screening telomerase inhibitors for treatment of
                                                                                                                                                                                                                      Example 1; Page 37-39; 44pp; Japanese.
98JP-0033584.
                                 (CHUS ) CHUGAI SEIYAKU KK.
                                                                  Tsuchiya M, Yoshida K;
                                                                                                  WPI; 1999-430393/36.
N-PSDB; AAX88251.
30-JAN-1998;
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. Search completed: November 12, 2003, 19:47:13 Job time : 33.6226 secs

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Sequence 134, App
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Sequence 67, Appl
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US-08-912-951-115
US-08-974-549A-13
US-08-912-951-13
US-08-912-951-13
US-08-912-951-10
US-08-912-951-10
US-08-912-951-317
US-08-912-951-317
US-08-912-951-317
US-08-912-951-317
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US-08-912-951-317
US-08-912-951-317
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-08-851-843A-225
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US-08-854-050-225
US-09-430-323-225
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US-09-675-321-2
                                                                                                                                                                                                                                                                                                                                                                           1 ARTFRREKRAERLTSRVKALFSVLNYE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328717 seqs, 42310858 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                   US-08-854-050-114
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Match Length
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1132
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No.
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2, Appli
611, App
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Sequence
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Sequence
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Sequence
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Sequence
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     Sequence
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Patent No. 6093809

GEMERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
US-09-052-919-2
US-08-912-951-2
US-08-912-951-32
US-08-912-951-323
US-08-912-951-325
US-08-912-951-325
US-08-912-951-325
US-08-912-951-324
US-08-912-951-334
US-08-912-951-334
US-08-912-951-314
US-08-912-951-314
US-08-912-951-314
US-08-912-951-314
US-08-914-549A-267
US-08-914-549A-604
US-08-914-549A-604
US-08-914-549A-604
US-08-914-549A-604
US-08-914-549A-604
US-08-914-549A-604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-020
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 114:
                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIPICATION OF ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
STATE: California
COUNTRY: United States of America
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Gaps
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ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California COUNTRY: United
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 4.5e-13;
Matches 27; Conservative 0; Mismatches 0;
               PRICE APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-0CT-1997
ATTORNEY AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
RELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 234:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chapman, Karen B.
APPLICANT: Morlin, Greegg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ARTFREKRAERLISRVKALFSVLNYE 27
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 114, Application US/08854050 Patent No. 6261836 GENERAL INFORMATION:
APPLICANT: Cech, Thomas R. APPLICANT: Lingner, Joachim APPLICANT: Chapman, Karen B. APPLICANT: Chapman, Karen B.
FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
HOLECULE TYPE: peptide
US-08-974-549A-234
                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid STRANDEDNESS:
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APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Moxin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Milliam H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
CORPRESSIONENCES: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:

OFFWAREL PATENTING SYSTEM:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
RIOR APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
FILING DATE: 01-OCT-1996
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
FILING DATE: 05-MAY-1997
FILING DATE: 06-MAY-1997
FILING DATE: 06-MAY-1997
FILING DATE: 09-MAY-1997
FILING DATE: 09-MAY-1997
FILING DATE: 09-MAY-1997
FILING DATE: US 08/851,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO PCT/US97/17618
                                                                                                                                                                                                                                                                                          1 ARTFREKRAERLTSRVKALFSVLNYE 27
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PRIOR DATE: 14-AUG-1997
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/915,503
PRIOR APPLICATION NUMBER: H-AUG-1997
PRING BATE: 14-AUG-1997
PRIOR APPLICATION DATE:
APPLICATION NUMBER: WO PCT/US97/176:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: U4-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION ATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 234, Application US/08974549A
Patent No. 6164178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                    LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                               Query Match
Best Local Similarity 100.0
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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: USA
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US-08-974-549A-234
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APPLICANT: Linguer, Joachim
APPLICANT: Linguer, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND TITLE OF INVENTION: THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                 Length 27;
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COUNTRY: Unitc.
ZIE: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODEFATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION HANDER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION HANDER: US 08/851,843
FILING DATE: 06-MAY-1997
STILING DATE: 06-MAY-1997
FILING DATE: 06-MAY-1997
TUTLOR DATE: 06-MAY-1997
TOTAL APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
TOTAL APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
TOTAL APPLICATION DATA: US 08/851,843
FILING DATE: 06-MAY-1997
TOTAL APPLICATION DATA: US 08/851,843
                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 130; DB 4;
Best Local Similarity 100.0%; Pred. No. 4.5e-13;
Matches 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, 8th Floor
                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 114:
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ARTFRREKRAERLISRVKALFSVLNYE 27
                                                                                                                                                                                                                                                                                                                                                                                                             1 ARTFRREKRAERLTSRVKALFSVLNYE 27
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APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
          TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 115, Application US/08912951
Patent No. 6475789
                          TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
                                                                                                                                   TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                         LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         San Francisco
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CLASSIFICATION:
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COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION *CUNKnown>
PRIOR APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: US OF MAY-1997
APPLICATION NUMBER: US 08/8724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 130; DB 3; Length 27; Best Local Similarity 100.0%; Pred. No. 4.5e-13; Matches 27; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andrews, William H.
DF INVENTION: No. 6309867el Telomerase
OF SEQUENCES: 225
                                                                    NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ARTFREKRAERLTSRVKALFSVLNYE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ARTFREKRAERLTSRVKALFSVLNYE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 114, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
NAkamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
01-OCT-1996
N: 536
                                               ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: California
                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                    TYPE: amino acid STRANDEDNESS:
                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                     US-08-854-050-114
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Length 129;
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APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Andrews, William H.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
                                                                                                                                                                                                                                                                                                                                               LOCATION: 1..129

COTHER INFORMATION: /note= "TRT motifs from human"

US-08-851-843A-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA ZIP: 94111-3834 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/974,549A FILING DATE: 19-NOV-1997 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 130; DB 3;
100.0%; Pred. No. 2.6e-12;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 ARTFREKRAERLISRVKALFSVLNYE 127
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-007-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
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APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAX-1997
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAX-1997
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRICE APPLICATION NUMBER: US 08/911,312
PRICE APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRICE APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
                                                                                               LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 100.v
                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                     NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-974-549A-13
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Best Local Similarity 100.0%; Pred. No. 4.5e-13;
Matches 27; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA.

APPLICATION NUMBER: US/08/851,843A

FILING DATE: 06-MAY-1997

CLASSIFICATION:

APPLICATION:

REAL OF THE CAME OF THE CAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ARTFRREKRAERLISRVKALFSVLNYE 27
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               California
: United States of America
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-912-951-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              쉽
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Peptide

COCATION: 1..129

JOTHER INFORMATION: /note= "TRT motifs from human"

US-08-854-050-67
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ADDRESSE: Townsend and Townsend and Crew STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 130; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 27; Conservative 0; Mismatches 0;
                                               FILING DATE: 25-APR-1997
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/644,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEFACOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 29-Oct-1999
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/430,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 ARTFRREKRAERLTSRVKALFSVLNYE 127
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                       MBER: US 08/846,017
25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 67, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakamura, Toru
Chapman, Karen B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 129 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-09-430-323-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 130; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California COUNTRY: United States of America
                                          APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA: O1-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randclph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEFAN: (415) 576-0200
TELEFAN: (415) 576-0300
INPORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 ARTFREEKRAERLTSRVKALFSVLNYE 127
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-WAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 67, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Greeg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 129 amino acide TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
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| Patent No. 6166178
| GENERAL INPORMATION:
| GENERAL INPORMATION:
| APPLICANT: Cech, Thomas R.
| APPLICANT: Chapman, Karen B.
| APPLICANT: Chapman, Karen B.
| APPLICANT: Harley, Calvin B.
| APPLICANT: Harley, William H.
| TITLE OF INVENTOR: William Hear Telomerase Catalytic Subunit NUMBER OF SEQUENCES: 727
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Two mean and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Peptide

// LOCATION: 1..129

// COTHER INFORMATION: /note= "TRT motifs from human"

US-08-912-951-13
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BEN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 130; DB 4; 100.0%; Pred. No. 2.6e-12;
                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION WINBER: US 08/724,643
FILING DATE: 10-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION UNMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
RECISTRATION NUMBER: 36,429
RECISTRATION NUMBER: 36,429
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 ARTFREKRAERLTSRVKALFSVLNYE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ARTFRREKRAERLTSRVKALFSVLNYE 27
              MBER: US 08/851,843
06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
                   APPLICATION NUMBER: PILING DATE: 06-M2 CLASSIFICATION: 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Sequence 13, Application US/08912951

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cach, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Kregg B.
APPLICANT: Mariew, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELCHERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND TITLE OF INVENTION: THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: /note= "TRT motife from human" SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
PTING DATE: 14-AUG-1997
                                                                                                                                                                                                NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
              FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
APPLICATION NUMBER: US 08/724,643
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 ARTFRREKRAERLISRVKALFSVLNYE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ARTFRREKRAERLTSRVKALFSVLNYE 27
                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1.129
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-430-323-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-912-951-13
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Gaps

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HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
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CTHER INFORMATION: /note= "protein encoded by clone 712562"
US-08-912-951-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 259;
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                                                                                                                                                                                                                                                                 COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
TITLE OF INVENTION: HUMAN TELOWERASE CATALYTIC STILL OF INVENTION: THERAPEUTIC METHODS NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 130; DB 4;
100.0%; Pred. No. 5.8e-12;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 ARTFREEKRAERLTSRVKALFSVLNYE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                        PAPPLICATION NUMBER: US/08/912,951
CLASSIFICATION NUMBER: US/08/912,951
CLASSIFICATION DATA:
APPLICATION NATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION: 435
                                                                                                                                                                                                                        United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-974-549A-603
; Sequence 603, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION: (415) 576-0200

TELEFAX: (415) 576-0200

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 259 pm<sup>2</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 259 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                               CITY: San Francisco
STATE: California
COUNTRY: United St
ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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; LOCATION: 1..259
; OTHER INFORMATION: /note= "protein encoded by clone 712562"
US-08-974-549A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 259;
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100.0%; Score 130; DB 3;
Best Local Similarity 100.0%; Pred. No. 5.8e-12;
Matches 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                           APPLICATION UNDBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION UNDBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION UNDBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REPERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         015389-002610US
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                                                                          APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/08912951; Patent No. 6475789; GENERAL INFORMATION: APPLICANT: Cech, Thomas R. APPLICANT: Lingner, Joachim, APPLICANT: Nakamura, Toru APPLICANT: Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Morin, Gregg B.
Harley, Calvin
Andrews, William H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 259 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-912-951-10
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
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LOCATION: 1..530
OTHER INFORMATION: /note= "fusion protein composed of
                        APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA

ZIP: 94111-1934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: U-OCT-1996
FRIOR APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 10-OCT-1997
FILING DATE: 10-APR-1997
FRIUM DATE: 25-APR-1997
FRIUM DATE: 25-APR-1997
FRIUM DATE: US 08/851,843
FRIUM DATE: US 08/911,312
FRIUM APPLICATION NUMBER: US 08/912,951
FRIUM APPLICATION NUMBER: US 08/915,503
FRIUM DATE: US 08/915,503
FRIEFRAM: US 08/915,503
                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend and Crew LL STREET: Two Embarcadero Center, Elghth Floor CITY: San Francisco STATE: California
Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

APPLICANT: Lingaper, Joachim
APPLICANT: Lingaper, Joachim
APPLICANT: Adamura, Toru
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Harley, William H.
TITLE OF INVENTION: THERAPEUTIC METHODS
TITLE OF INVENTION: THERAPEUTIC METHODS
OORRESPONDENCES A335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                ..
0
                           thrombin cleavage sequence, recognition sequence for heart muscle protein finase, residues introduced by cloning, eight consecutive His residues and hTRT protein fragment"
                                                                                                                                                                                                                                                           100.0%; Score 130; DB 3; Length 530; 100.0%; Pred. No. 1.3e-11; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      341 ARTFREKRAERLTSRVKALFSVLNYE 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco Center, Bun
CITY: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BARENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION ATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION 435
PRIOR APPLICATION ATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 25-APR-1997
CLASSIFICATION ATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION ATA:
APPLICATION NUMBER: US 08/44,419
FILING DATE: 18-APR-1997
CLASSIFICATION WHERE: US 08/724,643
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                             1 ARTFREEKRAERLTSRVKALFSVLNYE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 317, Application US/08912951
Patent No. 6475789
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 27; Conservative
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                    ;
US-08-974-549A-603
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US-08-912-951-317
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 130; DB 3; 100.0%; Pred. No. 2.1e-11;
FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 0.0-CCT-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 0.0-CCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 015389-002610US

FELERANCE/DOCKET NUMBER: 015389-002610US

TELEPANCH (415) 576-0200

TELEFAX: (415) 576-0300

ITELEPAX: (415) 576-0300

ITELEPAX: (415) 576-0300

TELEFAX: (415) 576-0300

TELEFAX: AND SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 807 amino acid

TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: November 12, 2003, 19:53:27 Job time : 12.566 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             642 ARTFREKRAERLTSRVKALFSVLNYE 668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Marches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-974-549A-5
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Sequence 5, Application US/08974549A

Patent No. 6166178

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Maramra, Toru
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SECUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                               100.0%; Score 130; DB 4; Length 530; 100.0%; Pred. No. 1.3e-11;
                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/974,549A
FILING DATE: 19-NOV-1996
PRIOR APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION NUMBER: US 08/844,419
FILING DATE: 25-APR-1997
PRIOR APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION NUMBER: US 08/846,017
PRIOR APPLICATION NUMBER: US 08/846,017
PRIOR APPLICATION NUMBER: US 08/846,017
PRIOR APPLICATION NUMBER: US 08/845,017
PRIOR APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          341 ARTFRREKRAERLTSRVKALFSVLNYE 367
                                                                                                                                                                                                                                                                                                                                                                             1 ARTFRREKRAERLTSRVKALFSVLNYE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PELICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
                            TELEFAX: (415) 576-0300
| INFORMATION FOR SEQ ID NO: 317:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 330 amino acids
| TYPE: amino acid
| TYPE: amino acid
| TOPOLOGY: linear
| MOLECULE TYPE: protein
| US-08-912-951-317
          (415) 576-0200
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
       TELEPHONE:
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US-08-974-549A-5
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GenCore version.5.1.6 Copyright. (c):1993% 2003 Compugen Ltd.
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Run on:

November 12, 2003, 19:41:59; Search time 4.98113 Seconds (without alignments) 226.583 Million cell updates/sec

US;08-854-050-112 131 1 FFYVTETTFQKNRLFFYRKSVWSK 24

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 segs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | , , , , , , , , , , , , , , , , , , , | nescription | 014746 homo sapien | 070372 mus musculu | O13339 schizosacch | | O00939 euplotes ae | ω. | P98005 thermus the | Q46803 escherichia | _ | | 2 arabidops | | | | Q04454 bacillus fi | P52386 human herpe | | H | | 'n | 'n | | | | | σ. | | P26561 bluetongue | drosoph | P56690 thermus the | | ~; | P03483 influenza a |
|-----------|---------------------------------------|-------------|--------------------|--------------------|--------------------|------------|--------------------|------------|--------------------|--------------------|------------|-----|-------------|------|------|------------|--------------------|--------------------|------------|------------|-----------|------------|------------|----------|--------------|------------|-----------|-----------|-----|-------------------|---------|--------------------|------|------|--------------------|
| SUMMARIES | Ę | | TERT HUMAN | | TERT_SCHPO | TERT_OXYTR | | TERT_TETTH | CO13_THETH | YGEW_ECOLI | CYOB_BUCAP | | | | | DYHC_SCHPO | YCT2_BACFI | UL24_HSV7J | YHIL ECOLI | ADF2_PETHY | ADF LILLO | OM22_NEUCR | CAKB_CANFA | CAKB RAT | . CCSA_TOBAC | COAA_RHIME | VP7_BTV10 | VP7_BTV17 | | VP7_BTV2A | LLON . | SYI_THETH | | | NRAM_IAUDO |
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| | Length | 1000 | 1132 | 1122 | 988 | 1132 | 1031 | 1117 | 791 | 363 | 629 | 662 | 146 | 420 | 663 | 4196 | 385 | 239 | 535 | 143 | 139 | 154 | 190 | 190 | 313 | 331 | 349 | 349 | 349 | 349 | 382 | 2 | 3 | 469 | 469 |
| de | Query | | | è. | m | 52.7 | | œ | 35.9 | വ | | | 34.7 | 34.4 | 34.4 | 34.4 | 4 | m. | ë. | 33.5 | 32.4 | 32.1 | 2 | ~ | ς. | ά. | ς. | | ς. | · . | ٠ | 32.1 | 31.7 | 31.7 | 31.7 |
| | ar COS | | 131 | 126 | 70 | 69 | 99 | 63 | 47 | 46 | 46 | 4 | 45.5 | 45 | 45 | . 45 | 44.5 | 44 | 4 | ش | 42.5 | 42 | 42 | 42 | 42 | 42 | 42 | 42 | 42 | 42 | 42 | 42 | 41.5 | 41.5 | 41.5 |
| | Result | | 7 | 7 | m | 4 | S | 9 | 7 | ∞ ` | σ. | 10 | 11 | 12 | 13 | 14 | 15 | ·16 | 17 | 18 | 19 | 50 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | | 29 | 30 | 31 | 35 | 33 |

| P03482 influenza a | Q9fvi2 petunia hyb | Q28067 bos taurus | Q16558 homo sapien | P38459 marchantia | Q33134 saxifraga o | Q9jt82 neisseria m | Q9jya0 neisseria m | PS8151 astasia lon | P38153 saccharomyc | 045436 caenorhabdi | |
|--------------------------|--------------------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--|
| NRAM_IAVI7 NRAM_IAZHS | ADF1 PETHY | CAKB_BOVIN | CAKB HUMAN | YM16 MARPO | MATK_SAXOP | TRMA NEIMA | TRMA_NEIMB | YCXC ASTLO | APM3 YEAST | NHR4_CAEEL | |
| | ı ~ | Ħ | П | - | - | - | - | П | - | 1 | |
| 469 | 139 | 190 | 190 | 244 | 352 | 362 | 362 | 426 | 483 | 492 | |
| 31.7 | 31.3 | 31.3 | 31.3 | 31.3 | 31.3 | 31.3 | 31.3 | 31.3 | 31.3 | 31.3 | |
| 41.5 | 41 | 41 | . 41 | 41 | 41 | 41 | 41 | 41 | 41 | 41 | |
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ALIGNMENTS

This SWISS-PROT entry is copyright. It is produced through a collaboration

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EMBL;
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcelor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     min, 20,0005696; C:telomere, TAS.
GO; GO:0003721; F:telomeric template RNA reverse transcriptas. . .; TAS.
GO; GO:0007031; P:telomere binding; TAS.
InterPro; IPR000477; RVIse.
InterPro; IPR003545; Telomerase_RT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TERT MOUSE STANDARD; PRT; 1122 AA.
070372; 035432;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FRB-2003 (Rel. 41, Last annotation update)
Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fransferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homolog.", Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases. Submitted OCT-1997) to the EMBL/GenBank/DDBJ databases. -!- FUNCTION: TELOMERASE IS. A RIBONUCLEOPROTEIN ENZYME ESSENTIAL THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98241176; PubMed=9582020; Greenberg R.A., Allsopp R.C., Chin L., Morin G.B., DePinho R.A.; "Expression of mouse telomerase reverse transcriptase during development, differentiation and proliferation."; Oncogene 16:1723-1730(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Martin-Rivera L., Herrera E., Albar J.P., Blasco M.A.; "Expression of mouse telomerase catalytic subunit in embryos and adult tissues.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 131; DB 1; Length 1132; 100.0%; Pred. No. 1.2e-12;
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1132 AA; 126996 MW; 94E35469C4CA33A0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> G (IN REF. 2)
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                                                                                                                                                                                                                                                                                       EMBL; AF128894; AA330037.1; -.
EMBL; AF128893; AAD30037.1; JOINED.
EMBL; AYOO7685; AAD33289.1; -.
BIR; TO3844; TO3844.
Genew; HGNC:11730; TERT.
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                                                                                                                                                                                                                             EMBL; AF015950; AAC51672.1; -. EMBL; AF018167; AAC51724.1; -.
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PRINTS; PR01365; TELOMERASERT.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01365; TELOMERASERT.
Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE=21848401; PubMed=11859360; Mood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A. Sgouros J., Peat N., Hayles J., Basham D., Bowman S., Brookn D., Bowman S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Horneby T., Howarth S., Huckle E.J., Hunt S., Jagels K. James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mugall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                               SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
-!- SUBGINIT: Interacts with PINX1 (By similarity).
-!- SUBGINIT: BELOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
TELOMERASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1122;
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; F85266905DD6558C CRC64;
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Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomycetales; Schizosaccharomycetaceae;
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Best Local Similarity 91.7%; Pred. No. 7.2e-12;
Matches 22; Conservative 2; Mismatches 0;
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InterPro; IPR000477; RVTse.
InterPro; IPR003545; Telomerase_RT.
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127977 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF051911; AAC09323.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB84200.1; -.
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1122 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TERT_SCHPO (013338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
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subunit) (Telomerase subunit P133)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                     Oxytricha trifallax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                         NCBI_TaxID=5946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=5940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; T31107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    telomerase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-binding.
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000939;
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Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

A Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Meltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

Meltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

Meltjens I., Vanstreels E., Holzer E., Moestl D., Hilbert H.,

Medre E., Elmermann W., Wedler H., Reinhardt R., Purnelle B.,

Goffeau A., Cadieu E., Dreanc S., Gloux S., Lelaure V., Mortier S.,

M. Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A.,

M. Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Foreburg S.L.,

R. Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,

"The genome sequence of Schizosaccharomyces pombe.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISOId=013339-2; Sequence-VSP 006395;
MISCELLANEOUS: DELETION CAUSES TELOMERE SHORTENING AND SENESCENCE.
SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
TELOMERASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                              FINCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR ELONGATES TELOMERASE IS A REPRINTI IN MOST EUKARYOTES. IT ELONGATES TELOMERES. IT A REVERSE TRANSCRIPTASE THAT ADDS SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO1365; TELOWERASERT.
Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
DNA-binding; Alternative splicing.
VARSPLIC 524 K -> KQ (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.4%; Score 70; DB 1; Length 988; 45.5%; Pred. No. 0.0038; tive 7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
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988 AA; 116328 MW; AB2DC7030228F443 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=013339-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            443 FFYITESSDLRNRTVYFRKDIW 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GeneDB SPombe; SPBC29A3.14c; -
InterPro; IPR000477; RVTse.
InterPro; IPR003545; Telomerase_RT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Nuclear. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FFYVTETTFOKNRLFFYRKSVW 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AF015783, AAC49802.1;
EMBL, AF015783, AAC49803.1;
EMBL, AL022299, CAA18391.1;
PIR, T03838; T03838.
                                                                                                                                                                                                                                                                                                                                                                                  Nature 415:871-880(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00078; rvt; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 10; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TERT OXYTR
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       SOTTING SOURCE COURSE SERVING SOURCE SERVING SOURCE SERVING SERVING SOURCE SERVING SERVING SOURCE SERVING SOURCE SERVING SOURCE SERVING SERVI
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                                                                                                                                                                                                                               ENYAN T.W., Sperger U.W., Chapman K.B., Cech T.R.;
"Telomerase reverse transcriptase genes identified in Tetrahymena thermophila and Oxytricha triffallax.";
"Telomerase reverse transcriptase genes identified in Tetrahymena thermophila and Oxytricha triffallax.";
-!- RUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR THE REPLICATION OF CHROMOSOME TERMINI IN MOST BUKARYOTES. IT ELONGATES TELOMERES. IT IS A REVENSE TRANSCRIPTASE THAT ADDS SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE SUGCELLULAR LOCATION: Nuclear.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
TELOMERASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCIENCE 276:561-567(1997).

-!- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUGARYOTES. IT ELONGATES TELOMBRES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE SEQUENCE MITHIN THE RNA COMPONENT OF THE ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit) (Telomerase subunit P123).
Eukaryota, Alveolata, Ciliophora, Spirotrichea, Stichotrichia,
Stichotrichida, Oxytrichidae, Oxytricha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Cech T.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euplotes aediculatus.
Eukaryota; Alveolata; Ciliophora; Spirotrichea; Hypotrichia;
Euplotida; Euplotidae; Euplotes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.7%; Score 69; DB 1; Length 1132;
43.5%; Pred. No. 0.0063;
Live 7; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Reverse transcriptase motifs in the catalytic subunit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1132 AA; 134124 MW; 81E145F5F24392DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1031 AA.
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Interpro; IPR003545; Telomerase_RT.
PRINTS; PR01365; TELOMERASERT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FFYVTETTFOKNRLFFYRKSVWS 23
                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=98337940; PubMed=9671703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97274210; PubMed=9110970;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
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les 10; Conservative
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EMBL; AF061284; AAC39140.1;
                                                                                                                                                                                     48.1
Best Local Similarity 42.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=274;
                                                                                                                                                                                                                                                                                                                                  THETH
                                                                                                                                                DNA-binding
                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                    CO13 THE P98005;
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                                                                                                                                                                                                                                                                                                                    CO13_THETH
                                                                                                                                                                                                                                                                                                         RESULT
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                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The reverse transcriptase component of the Tetrahymena telomerase ribonucleoprotein complex."; 95:8485-8490(1998).

Proc. Natl. Acad. Sci. U.S.A. 95:8485-8490(1998).

-! FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR ELOMERASE IT IS A REVERSE TRANSCRIPTASE THAT ADDS ELOMETES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Terrahymena thermophila.
Tebraryota: Alveolata: Ciliophora; Oligohymenophorea: Hymenostomatida:
Tetrahymenina; Tetrahymena.
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
                                                                                                                                                                                                                       PRINTS; PR01365; TELOMERASERT.
Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98337940; PubMed=9671703;
Bryan T.M., Sperger J.M., Chapman K.B., Cech T.R.;
Bryan T.M., Sperger J.M., Chapman K.B., Cech T.R.;
"Telomerase reverse transcriptase genes identified in Tetrahymena
"Helomerase reverse transcriptase genes identified in Tetrahymena
                                                                                                                                                                                                                                                                                                                  .;
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                                                                                                                                                                                                                                                                                Score 66; DB 1; Length 1031;
Pred. No. 0.017;
6; Mismatches 6; Indela
SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY: TELOMERASE SUBFAMILY.
                                                                                                                                                                                                                                                               1031 AA; 122562 MW; 57B87A63A1FED60F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 95:8479-8484 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1117 AA.
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 45.5%; Pred. No. (
Matches 10; Conservative 6; Mismatch
                                                                                                                                                                                                                                                                                                                                                                455 FFYVTEQQKSYSKTYYYRKNIW 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subunit) (Telomerase subunit P133).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98337941; PubMed=9671704; Collins K., Gandhi L.;
                                                                                                                                                                                                                                                                                                                                                 1 FFYVTETTFOKNRLFFYRKSVW 22
                                                                                                                                                                          EMBL, U95964; AAC47515.1; -.
InterPro; IPR000477; RVTse.
InterPro; IPR003545; Telomerase_RT.
                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=5911;
                                                                                                                                                                                                                                                                                                                                                                                                                                               TERT TETTH 077448;
                                                                                                                                                                                                                                                               DNA-binding
                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                    TERT_TETTH
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
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Mather M.W., Springer P., Hensel S., Buse G., Fee J.A.;
Mather M.W., Springer P., Hensel S., Buse G., Fee J.A.;
Mather M.W., Springer P., Hensel S., Mucleotide
To Stringer Genes from Thermus thermophilus. Nucleotide
To Stringer Genes and III of cytochrome caa3.";
To Stringer Genes Genes To Stringer Genes G
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE HEMB-COPPER RESPIRATORY OXIDASE PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- COFACTOR: TWO HEME GROUPS AND COPPER B.
-!- PATHWAY: Respiratory chain; terminal step.
-!- SUBUNIT: POSSIBLY A HETERODIMER OF A-PROTEIN (CONTAINS: CYTOCHROME C OXIDABE SUBUNITS I AND III) AND SUBUNIT II. THE A-PROTEIN COULD ALSO PRESENT A PRECURSOR FORM OF SUBUNITS I AND III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Last sequence update)
Last sequence update)
Cytochrome c oxidase polypeptide I+III (EC 1.9.3.1) (Cytochrome c aa(3) subunit 1) (Cytochrome caa3) (A-protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Deinôcoccus-Thermus; Deinococci; Thermales; Thermaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.1%; Score 63; DB 1;
42.9%; Pred. No. 0.054;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Mismatches
                                                                                                                                                                                                                                                                                        PIR, T14891, T14891.
InterPro; IPR000477; RVTSE.
InterPro; IPR003545; Telomerase_RT.
Pfam; PF00078; rvt; 2.
PRNITS; PR01365; TELOMERASERT.
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STRAIN=HB8 / ATCC 27634;
MEDLINE=93194828; PubMed=8383670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||:|| : ::|:|| : 476 FYITEKHKEGSQIFYYRKPIW 496
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                                                                                                                                                                                 EMBL; AF062652; AAC39135.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ubiquinol oxidase polypeptida 1 (EC 1.10.3.-) (Cytochrome O subunit 1)
(Oxidase BO(3) subunit 1) (Cytochrome O ubiquinol oxidase subunit 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (by Similarly).

-!- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.

-!- COFACTOR: Contains two protoheme IX (heme BS5 and BS62) and copper B (By similarity).

-!- PATHWAY: Ubiquinol oxidase catalyzes the terminal step in the electron transport chain.

-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

-!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE=22004549; PubMed=12089438;
Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
"50 million years of genomic stasis in endosymbiotic bacteria.";
Science 296:3376-2376-2379(2002).

-! FUNCTION: Cytochrome O terminal oxidase complex is the component
of the aerobic respiratory chain that predominates when cells are
grown at high aeration. This ubiquinol oxidase shows proton pump
activity across the membrane in addition to the electron transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
           Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao. Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 363;
                                      "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
-!- SIMILARITY: SOME, TO ORNITHINE CARBAMOYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Complete proteome.
SEQUENCE 363 AA; 40212 MW; F8436BC00BF2DC83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                35.1%; Score 46; DB 1; 42.1%; Pred. No. 7.6; iive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          659 AA.
                                                                                                                                                                                                                                                     PIR, F65070; F65070.
BcoGene; EG13053; ygew.
InterPro; IPR006130; ASp/Orn Cotranf.
InterPro; IPR006131; OTCace O.
InterPro; IPR006132; OTCace O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321 VTEGVFEKYRIATYKEASW 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 VTETTFOKNRLFFYRKSVW 22
                                                                                                                                                                                                                          EMBL; U28375; AAA83051.1; -.
EMBL; AE000370; AAC75908.1; -.
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Best Local Similarity 42.1%;
Local 8; Conservative
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Q8K994;
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MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
IRON (HEME A AXIAL LIGAND) (PROBABLE)
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COPPER B (PROBABLE).
COPPER B (PROBABLE).
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
14Ppothetical protein ygew.
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 or send an email to license@isb-sib.ch)
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                                           PIR; A46616; A46616.
HSSP; P18401; 1FFT.
INTECPTO; IPR0000883; COXI.
Pfam: PF00115; COXI; 1.
Pfam: PF00115; COXI; 1.
Pfam; PF00115; COXI; 1.
                                                                                                                                      PRINTS; PRO1165; CYCOXIDASEI.
PRODOM; PRO00382; CYC_Oxdse_III; 1.
PROSITE; PS00077; COX1; 1.
PROSITE; PS50253; COX3; 1.
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269 STFARKPLFGYRQMVWAQ 286
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                             EMBL; M84341; AAA27485.1; -.
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Best Local Similarity 44.4°
Matches 8; Conservative
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                   NCBI_TaxID=118099;
                                    SEQUENCE FROM N.A.
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ubiquinol oxidase polypeptide I (EC 1.10.3.-) (Cytochrome O subunit 1)
(Oxidase BO(3) subunit 1) (Cytochrome O ubiquinol oxidase subunit 1).
Cyob OR BU471...-, (Annotation prisum) (Acytichosiphon pisum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                 CYTORIAND.

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC AXIAL LIGAND) (PROBABLE).

COPPER B (PROBABLE).

IRON (HEME O AXIAL LIGAND) (PROBABLE).

IRON (HEME B AXIAL LIGAND).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                1/-histidyl-3'-tyrosine (By similarity) 75028 MW; 23D6FB4B04732D23 CRC64;
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                                            EMBL, AE014121; AAM67998.1; -.
InterPro: IPR000883; COX1.
Pfam; PF00115; CXCOXIDASEI.
PROSITE; PS00077; COX1; 1.
PROSITE; PS00077; COX1; 1.
Oxidoreductase; Respiratory chain; Transmembrane; Heme; Copper;
                                                                                                                                                                                                                                                                                                                                                                                                                                          35.1%; Score 46; DB 1; Length 659; 56.2%; Pred. No. 14; 5.1ve 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
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Hydrogen ion transport; Complete proteome.
EXTRACELLULAR (POTENTIAL).
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Best Local Similarity 56.2.
Best Local 9; Conservative
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659 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
IRON (HEME B AXIAL LIGAND) (PROBABLE).
                                                                                                                                                                                                                                                    Buchnera SP. APS.";
Nature 407:81-266(2000).
Nature 407:81-266(2000).
OF THE ARROPHE O TERMINAL OXIDASE COMPLEX IS THE COMPONENT
OF THE ARROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE
OF THE ARROBIC RESPIRATORY CHAIN THAT PREDOMING PROTON PUMP
GROWN AT HIGH AERATION. THIS UBIQUINOL OXIDASE SHOWS PROTON PUMP
ACTIVITY ACROSS THE MEMBRANE IN ADDITION TO THE ELECTRON TRANSFER
                                                                                                                                                                                                                                                                                                                                                                                                              HSSP, P18401: 1FFT.

HSSP, P18401: 1FFT.

InterPro; 1PR001883; COX1.

Pfam, PF00115; COX1.

PRINTS; PR001165; CYCXIDASEI.

PROSTIE; P800077; COX1; 1.

POTENTIAL).

DOMAIN

1 35

POTENTIAL).
                                                                                                                                                                            MEDLINE=20445173; PubMed=10993077; Sakaki Y., Ishikawa H.;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
symbiotic bacterium).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CV. Columbia,
MEDLINE-20083487; PubMed=10617197,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Mofflat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                  1'-histidyl-3'-tyrosine (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COPPER B (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
IRON (HEME O AXIAL LIGAND) (PROBABLE)
IRON (HEME B AXIAL LIGAND) (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=cv. Columbia;
MEDLINE=21307188; PubMed=11414611;
MEDLINE=21307188; PubMed=11414611;
MEDLINE=21307188; PubMed=11414611;
"Molocular identification and characterization of the Arabidopsis AtADF1, AtADF5 and AtADF6 genes.";
Plant Mol. Biol. 45:517-527(2001);

    -!- PTM: Phosphorylated.
    -!- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.";
                                                                                                                             .
0
                                                                                                   35.1%; Score 46; DB 1; Length 662; 56.2%; Pred. No. 14;
                                                                                                                            6; Indels
                                                                               75455 MW; 3F502A628133EA65 CRC64;
                                                                                                                                                                                                                        ADF6 ARATH STANDARD; PRT; 146 AA. 092SKZ; 093VZ4; 09SJX6; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Actin-depolymerizing factor 6 (ADF-6) (AtaDF6).
                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                    304 TFSKKRLFGYVSLVWA 319
                                                                                                                                               8 TFQKNRLFFYRKSVWS 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 402:761-768(1999).
                                                                                                                        9; Conservative
 284
288
333
334
419
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284
662 AA;
                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
-!- TISSUE SPECIFICITY: NODULES.
-!- SIMILARITY: STRONG, TO E.COLI SBMA.
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Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
-!- FUNCTION: FUNCTIONS IN THE TRANSPORT OF MOLECULES, POSSIBLY
PEPTIDES, ACROSS THE INNER MEMBRANE. IS ESSENTIAL FOR BACTEROID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
34.7%; Score 45.5; DB 1; Length 146;
Best Local Similarity 39.1%; Pred. No. 3.5;
Matches 9; Conservative 5; Mismatches 6; Indels ...
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Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
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146 AA; 16708 MW; A97CEFSD2CC17A85 CRC64;
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PROSITE; PS00325; ACTIN DEPOLYMERIZING; FALSE NEG.
Actin-binding; Multigene family; Phosphorylation.
DOMAIN
99 118 ACTIN-BINDING (POTENTIAL)
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
BACA OR RBI125 OR SMB209999
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                                                         EMBL, AF102824; AAD09112.1; -.
EMBL, AF183576; AAF01035.1; -.
EMBL, AV005533; AAD20665.2; -.
EMBL, AV057719; AAL15349.1; -.
EMBL, AF372880; AAK49596.1; ALT_INIT.
HSSP; Q39250; 1F75.
send an email to license@isb-sib.ch)
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PRINTS; PR00006; COFILIN.
ProDom; PD002129; Actbind cofln; 1.
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79 FDFVTSENCQKSKIFFF---AWS 98
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MEDLINE=93339575; PubMed=8393417;
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Genes Dev. 7:1485-1497(1993)
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TOPOLOGY
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 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                          01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ubiquinol oxidase polypeptide I (EC 1.10.3.-) (Cytochrome O subunit i)
(Oxidase BO(3) subunit 1) (Cytochrome O ubiquinol oxidase subunit 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=KI2 / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMett G. III, Bloch C.A., Perna N.T., Burland V., Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K., Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                        Transport; Transmembrane; Inner membrane; Plasmid; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli,
Escherichia coli 06, and
Escherichia coli 0157:H7.
Escheria; Proteobacteria; Gammaproteobacteria; Enterobacteria;
Enterobacteriacea; Escherichia.
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STRAIN=06.HI, CETO73 / ATCC 700928;
MEDGLINE=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                        Score 45; DB 1; Length 420;
                                                                                                                                                                                                             6; Indels
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548496A86AD1D0FE CRC64;
                                                                                                                                                                                                                                                                                                          663 AA
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CYOB OR B0431 OR C0542 OR 20534 OR ECS0485.
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                                                EMBL, ALG03646; CAC49525.1; -. PIR; A47649; A47649. PIR; E95982; E95982.
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                                       EMBL; X73522; CAA51918.1; -.
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420 AA;
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nes 8; Conserv
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-!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
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Nat. Struct. Biol. 7:910-917(2000).

Nat. Struct. Biol. 7:910-917(2000).

-!- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT

-!- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COLI THAT PREDOMINATES WHEN

OF THE AEROBIC RESPIRATORY CHAIN OF E.COLI THAT PREDOMINATES SHOWS

CELLS ARE GROWN AT HIGH AERATION. THIS UBIQUINOL OXIDASE SHOWS
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ASP-75; HIS-98 AND GLN-101.
ANDLINE-20473233; PubMed=11017202;
Abramson J., Riistama S., Larsson G., Jasaitis A., Svensson-Ek M.,
Pubstinen A., Iwata S., Wikstrom M.;
Pubstinen A., Iwata S., Wikstrom M.;
"The structure of the ubiquinol oxidase from Escherichia coli and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=0157:H7 / RIMD 0509952;

NEDLINE=2115631; PubMed=11258796;
NEDLINE=2115631; PubMed=11258796;
NapulNE=21156321; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Tanaka M., Tobe T.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Siningawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
"Complete genome sequence of enterohemorrhagic secherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
"NA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chepuri V., Gennis R.B.; "The use of gene fusions to determine the topology of all of the subunits of the cytochrome o terminal oxidase complex of Escherichia
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R., "Extensive mosaic structure revealed by the complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.
-!- COFACTOR: CONTAINS TWO PROTOHEME IX (HEME B55 AND B562) AND COPPER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PATHWAY: UBIQUINOL OXIDASE CATALYZES THE TERMINAL STEP IN THE ELECTRON TRANSPORT CHAIN.
                                                                                                                                                                                                                                                                                                         MEDLINE-21074935, PubMed=11206551;
MEDLINE-21074935, PubMed=11206551;
Perma N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Perma N.T., Plunkett G. III, Burland V., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Dimalanta E.T., Potamousis K.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Melch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli O157:H7.";
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oxidase complex of
                                                                                                                                                                               of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
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Chepuri V., Lemieux L., Hill J., Alben J.O.,
"Recent studies of the cytochrome o terminal
Escherichia coli.";
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                                                                       EMBL; J05492; AAA33632.1; -

BERL; J05664; AAA73632.1; -

BERL; J02664; AAA7362.1; -

BERL; J02664; AAA77922.1; -

BERL; J02664; AAA77922.1; -

BERL; AB00252; AAG5470.1; -

BERL; AB002551; BAB33908.1; -

BERL; A95040; A85540.

BERL; A95040; A85540.

BERL; B90689; B90689.

BERL; B90689; B90689.

BECGene; EG10179; COX.1.

PERN; BACSONIS; COX.1, 1.

PRINTS; PR01165; CYCOXIDASEI.

PROSITE; PR01055; CYCOXIDASEI.

PROSITE; PR01055; CYCOXIDASEI.

PROSITE; PR01057; COX.1, 1.

CXIGOTEGUCASE; Respiratory chain; Transmembrane; Inner membrane; DOMAIN.

TRANSMEM 17 35 I.

TRANSMEM 17 35 I.

TRANSMEM 17 35 I.

PROMAIN.
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IRON (HEME B AXIAL LIGAND) (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
IRON (HEME O AXIAL LIGAND) (PROBABLE).
IRON (HEME B AXIAL LIGAND) (PROBABLE).
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R->L: ABOLISHES ENZYME ACTIVITY.
R->Q: ABOLISHES ENZYME ACTIVITY.
D->N: ABOLISHES ENZYME ACTIVITY.
H->N: ABOLISHES ENZYME ACTIVITY.
Q->N: REDUCES ENZYME ACTIVITY.
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| FT TURN 169 172 FT TURN 174 176 FT TURN 182 183 FT TURN 218 214 FT HELIX 227 224 FT HELIX 227 241 FT TURN 242 243 FT TURN 246 269 FT HELIX 200 214 FT TURN 246 269 FT HELIX 247 259 FT HELIX 247 259 FT HELIX 248 259 FT HELIX 258 258 FT HELIX 258 259 FT HELIX 258 258 FT HELIX 258 259 FT HELIX 258 | RESULT 14 DYHC SCHPO BYCSCHPO CO13290; O9P6L0; G9TDPB; T15-JUL-1998 (Rel. 36, Created) DT 15-JUL-1998 (Rel. 36, Last sequence update) CS CARAINS-CATOMANON SCOR SCHIZOSACCHATOMYCETS RA SEQUENCE FROM N.A. RA MODALINE=21848401; PubMed=11859360; RA MODALINE=21848401; PubMed=11859360; RA MODALINE=21848401; PubMed=11859360; RA BLOOKS K., Brown D., Brown S., Chillingworth T., Churcher C.M., RA BLOOKS K., Brown D., Brown S., Chillingworth T., Churcher C.M., | RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., RA Gentles S., Goble A., Hamilan N., Harris D., Hiddgson G., Holroyd S., Hornsby T., Howarth S., Hutcke E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Money P., Moule S., Munglal K., Murphy L., Niblett D., Odell C., Molle K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Skelton J., Simmonia M., Squares R., Squares R., Starens S., Stevens K., Starbot K., Taylor K.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Modward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Muller T., Whitehead S., Rabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Polt R. Berr P., Zimmernann W., Wedler H., Rainhardt R., Pohl T.M., Rabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Motier S., Motier S., Galbert F., Aves S.J., Xiang Z., Hunt C., Moert B., Motier S., Lorano S., Gloux S., Lelaure V., Motier S., Longer M., Gailbert F., Aves S.J., Xiang Z., Hunt C., Moere K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Bominguez A., Revuelta J.L., Moreno S., Armetrong J., Forsburg S.L., R. Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., R. Armetrong J., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; R. Nurse P.; |
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                                                                                                the inner plasma membrane, broken the inner plasma membrane browning the inner plasma membrane probably consist of an N-terminal stem the inner plasma membrane probably consist of an order of and interacts with other dynein components), (which binds cargo and interacts with other dynein six tandemly—and the head or motor domain. The motor contains a ring. A stank—like linked AAA domains in the head, which form a ring. A stank—like structure (formed by two of the colled coil domains) protrudes structure (formed by two of the colled coil domains) protrudes structure AAA and AAA and terminates in a microtubule-binding between AAA and ANA or so ontribute to this ring; it is not site. A seventh domain may also contribute to this ring; it is not site. A seventh domain may also contribute to this site; it is not site. A seventh domain so the C terminus forms this extra clear whether the N-terminus or the C terminus forms this extra sites, one per AAA domain. Probably only one of these (within AAA sites, one per AAA domain. Probably only one of these (within AAA actually hydrolyzes ATP), the others may serve a regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dynein; Microtubules; ATP-binding; Repeat; Coiled coil.
SUBDUNIT: Consists of at least two heavy chains and a number of intermediate and light chains. SUBCELLULAR LOCATION: Cytoplasmic. Probably binds indirectly to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 4196;
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01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
18-OCT-2001 (Rel. 40, Last annotation)
18-OCT-2001 (Rel. 28, Last annotation)
18-OCT-2001 (Rel. 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the dynein heavy chain family.
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AAA 1 (BY SIMILARITY).

AAA 2 (BY SIMILARITY).

AAA 3 (BY SIMILARITY).

AAA 4 (BY SIMILARITY).

AAA 5 (BY SIMILARITY).

AAA 6 (BY SIMILARITY).

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EMBL; AL35862; CAB90788.1; --
EMBL; AL132839; CAB60251.1; --
PIR; T43274; T43274
Geneb SPowbe; SPA(1093.06c; --
InterPro; IPR003593; AAA_ATPase.
SWART; SW00382; AAA; 3.
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Best Local Similarity 4/...
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Conservative
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                       Quirk P.G., Hicks D.B., Krulwich T.A.; "Cloning of the cta operon from alkaliphilic Bacillus firmus OF4 and "Cloning of the cta operon from alkaliphilic Bacillus firmus of the pH-regulated cytochrome caal oxidase it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                              encodes.";
J. Biol. Chem. 268:678-685(1993).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE UPF0118 (PERM) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44.5; DB 1; Length 385;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                            protein; Transmembrane
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                STRAIN=0F4;
MEDLINE=93107080; PubMed=7678007;
                                                                                                                                                                                                                                                                                                                                                                                                                                          43410 MW;
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InterPro; IPR002549; UPF0118.
Pfam; PF01594; UPF0118; 1.
Hypothetical protein; Transmen
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42.9%;
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Matches 9; Conservative
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191
255
276
304
350
385 AA;
SEQUENCE FROM N.A.
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O9spu7 arabidopsis

Q9ai29 carsonella P91812 toxocara ca Q9npt3 homo sapien Q8ibb4 plasmodium Q9avy9 guillardia Q8bxKo weddellina Q8bxKo weddellina Q8bxKo weddellina Q8bxXo mus musculu Q92112 mus musculu Q8f7t5 leptospira Q8f119 providencia Q8f7t1 leptospira Q8f119 providencia Q8f7t2 arabidopsis Q9df12 larcococcus Q94b13 ranbidopsis Q8x60 escherichia Q8bvn3 homo sapien Q9bvn3 homo sapien Q9bvn3 homo sapien Q91by2 shewanella Q8x57 yersinia pe

O9m594 elaeis guin O83801 treponema p

O95w37 arabidopsis O91nk8 arabidopsis Q9aqi7 streptococc

us-08-854-050-112.rspt

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Hisatomi H., Nagao K., Kanamaru T., Hirata H., Miyachi K., Hikiji H., "Exon 11 deleted variant of human reverse transcripatse."; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AB086950; BAC11015.1; EMBL, AB086950; BAC11015.1; PRO13545; Telomerase R. PRINTS; PR01365; TELOMERASER. PRINTS; PR01365; TELOMERASER. SEQUENCE 795 AA; 88965 MW; 6BEAC8A6D1A2E8CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
ABG-deleted variant of telomerase reverse transcriptase.
TERT
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Pred. No. 4.3e-12;
): Mismatches 0;
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                                                        P91812

09NPT3

09NPT3

09NPT3

09NT3

08KKC

08KRS

08YRS

09Z112

087T5

08YT6

08YT6

08YT6

08YT6

08YT6

08YT6

09YF7

09YF7

09FF91

09F
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O83801
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QBN6C3;
01-OCT-2002 (TrEMBLrel. 22,
  11123
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TISSUE=Stomach;
                                                                          NCBI_TaxID=9606;
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Matches
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28NG38
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Q81kw0 oryza sativ
Q8muga paramecium
Q9grc5 paramecium
Q9grc5 paramecium
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Q9da32 xenopus lae
Q9r0b3 mus musculu
Q8i8z6 sterkiella
Q8i8z7 sterkiella
Q8sqq0 encephalito
Q8mub3 euplotes cr
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Q8n6c3 homo sapien
Q8ng46 homo sapien
Q9jk99 rattus norv
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                                                                                                                      November 12, 2003, 19:42:29 ; Search time 22.9434 Seconds (without alignments) 269.937 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                830525 segs, 258052604 residues
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1 FFYVTETTFQKNRLFFYRKSVWSK 24
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                                                                              OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Q8N6C3
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Q9JK99
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Q9QXZ4
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Maximum DB
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Gaps

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Length 795; Indels

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Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                            PRT; 1128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochim, Biophys. Acta 1517:398-409 (2001)
EMBL, AF149012; AAF17334.1; -
InterPro; IPR000477; RVISe.
InterPro; IPR003545; Telomerase_RT.
                                                                                                                                                                  PRINTS; PR01365; TELOMERASERT
RNA-directed DNA polymerase; Transferase.
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Interpro; IPR003545; Telomerase_RT
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                                              NCBI_TaxiD=10116;
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Q9DE32
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                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                            Kazumasa H.:
"Both beta and gamma deletion isoform of human telomerase reverse
                                                                                    Homo sapiens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 131; DB 4; Length 1069;
Pred. No. 5.7e-12;
                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                            100.0%; Score 131; DB 4; Length 807; 100.0%; Pred. No. 4.4e-12; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hisatomi H., Nagao K., Hirata H., Hikiji K., Kanamaru T., "Exon 11 deleted variant of the human telomerase reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcriptase.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB085628; BAC11010.1.; -.
InterPro; IPR003545; Telomerase_RT.
PRINTS; PR01365; TELOMERASERT.
RNA-directed DNA polymerase.
SROUENCE 1069 AA; 120047 MW; BEIE77A653B1C666 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                       transcriptase.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB086379; BAC11014.1; -.
InterPro; IPR003545; Telomerase_RT.
PRINTS; PR01365; TELOMERASERT.
SEQUENCE 807 AA; 90225 MW; 199664460CE6D763 CRC64;
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                            01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Beta and gamma deletion isoform of telomerase reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-CCT-2002 (TrEMBLrel. 22, Created)
01-CCT-2002 (TrEMBLrel. 22, Last sequence update)
01-CCT-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Telomerase reverse transcriptase
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Query Match
Best Local Similarity 100.0%;
Matches 24; Conservative 0;
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                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=Stomach cancer;
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Matches 24; Conserv
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01-MAR-2003
                                                                           transcriptase.
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                                                                                                                                                                                                                                                                                   SEQUENCE
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Q8NG46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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Local Similarity 91.7%; Pred. No. 1.9e-11;
hes 22; Conservative 2; Mismatches 0; Indels
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Wong S., Gao S., Xu X., Yu H.;
"Rat telomerase catalytic subunit, rTERT.";
submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF247818; AF62177.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Telomerase reverse transcriptase.
                                                                                                                                                                                                                                                                                       SEQUENCE 575 AA; 65672 MW; F80C81BD7F6A91A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2002 (TrEMBLrel. 22, Last annotation update)
10-CCT-2002 (TrEMBLrel. 22, Last annotation update)
Telomerase catalytic subunit.
Mesocricetus auratus (Golden hamster).
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Gaps

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Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P., Welbac F., El Alaoui H., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P.; "Genome sequence and gene compaction of the eukaryote parasite Encephalitozoon cuniculi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Encephalitozoon cuniculi.
Eukaryota, Fungi, Microsporidia, Unikaryonidae, Encephalitozoon.
NCBI_TaxID=6035,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Alveolata, Ciliophora, Spirotrichea, Stichotrichia,
Stichotrichida, Oxytrichidae, Sterkiella.
NCBI_TaxID=200599;
                                                                                                                                                                                        Length 1108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Match 52.7%; Score 69; DB 5; Length 1135; Local Similarity 43.5%; Pred. No. 0.033; les 10; Conservative 7; Mismatches 6; Indels
                                             Stichotrichous ciliates.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY116502; AAN87867.1; ...
NON TER
1 SEQUENCE 1108 AA; 131535 MW; EC8262E01B8E0FAD CRC64;
                                  macronuclear telomerase gene in two closely related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stichotrichous ciliates.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY116501; AAN87866.1; -.
SEQUENCE 1135 AA; 1343141 MW; 3661E5D9300A4942 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marandi S.S., Prescott D.M.; "The macronuclear telomerase gene in two closely related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genoscope;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Last annotation update)
                                                                                                                                                                               Ouery Match 52.7%; Score 69; DB 5; Best Local Similarity 43.5%; Pred. No. 0.033; Matches 10; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1135 AA.
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535 YFYSTEKAKEYQRIFYYRKNIWN 557
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01-07UN-2002 (TrEMBLrel. 21, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
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562 YFYSTEKAKEYQRIFYYRKNIWN 584
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01-JUN-2002
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Matches
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Q8SQQ0
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Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drissi R., Cleveland J.L.;
"Sequence of a Mus musculus telomerase catalytic subunit intron.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF090439; AAD54013.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Sterkiella sp. Aspen.
Bukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
Stichotrichida; Oxytrichidae; Sterkiella.
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                                                                                                                                                                                                                                                                          InterPro; Leavest 2.
Pram; PRO0078; rvt; 2.
PRINTS; PRO1055; TELOMERASERT.
RNA-directed DNA polymerase; Transferase.
1191 AA; 138016 MW; 9BD9D776869A57D6 CRC64;
                                                                                                                                    SEQUENCE FROM N.A.

Kuramoto M., Ishikawa F.;

Kuramoto M., Ishikawa F.;

Kuramoto M., Ishikawa F.;

Submitted (GEC-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF212299; AAG43537.1;

InterPro; IPR000477; RVTse.

InterPro; IPR001545; Telomerase_RT.
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52 AA; 6479 MW; 41473425E44BDA9C CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 23, Last annotation update)
Telomerase reverse transcriptase.
Paramecium tetraurelia.
Eukaryota: Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Nagnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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50.0%; Pred. No. 0.23;
ative 5; Mismatches 6; Indels C
                                                                                                                                                                                                                                                                                                    Query Match 48.9%; Score 64; DB 10; Length 1259; Best Local Similarity 50.0%; Pred. No. 0.23; Matches 11; Conservative 5; Mismatches 6; Indels
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PROSITE; PSO0527; RIBOSOMAL S14; 1.
RNA-directed DNA polymerase; Transferase.
SEQUENCE 1261 AA; 143715 MW; 353153D1C8B7D5CB CRC64;
                                                                                           Pfam; PF00078; rvt; 2.
PRINTS; PR01365; TELOMERASERT.
PROSITE; PR01365; RIBOSOMAL S14; 1.
PROSITE; PR0157; RIBOSOMAL S14; 1.
RNA-directed DNA polymerase; Transferase.
SEQUENCE 1259 AA; 143710 MW; 15B041789F2D5CAD CRC64;
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01-00T-2002 (TrEMBLrel. 22, Last sequence update)
01-0MT-2003 (TrEMBLrel. 23, Last annotation update)
11-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Telomerase reverse transcriptase.
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Interpro; IPR000477; RVTse.
Interpro; IPR003545; Telomerase_RT.
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Interpro; IPR001209, Ribosomal_S14.
Interpro; IPR000477; RVISe.
Interpro; IPR003545; Telomerase_RT.
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EMBL; AF494453; AAM21641.1; -.
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Matches 11; Conservative
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овмиов;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                     Gaps
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Euplotida; Euplotidae; Moneuplotes.
NCBI_TaxID=5936;
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1 Similarity 45.5%; Pred. No. 0.19; 7; Indels
10; Conservative 5; Mismatches 7; Indels
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PÉAMTS, PF0001365; TELOMERASERT.
RNA-directed DNA polymerase; Transferase.
SEQUENCE 1032 AA; 122966 MW; 0C401515839801A8 CRC64;
                                                                                                                                                                                                                                                                                 Length 823;
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                          Nature 414:450-453(2001).

EMBL; AL590451; CAD27002.1; -.

InterPro; IPR000477; RVTse.

Pfam; PP0078; rvt; 1. rvt; 1. rxt; 1. rxt; 1. RNA-directed DNA polymerase; Transferase.

RNA-directed DNA polymerase; Transferase.

SEQUENCE 823 AA; 95280 WW; 8FD1BED4CCE68354 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                     Score 65; DB 5;
Pred. No. 0.1;
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40.9%; Pred. No. v.-.
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|FYVTEQQKSYSETYYYRKNIW 476
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InterPro; IPR003545; Telomerase_RT.
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                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 40.9%
watches 9; Conservative
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A Takenaka Y., Matsuura T., Haga N., Mitsui Y.;

A Takenaka Y., Matsuura T., Haga N., Mitsui Y.;

B Matsuara T., Haga N., Mitsui Y.;

Takenaka Y., Matsuura T., Haga N., Mitsui Y.;

Takenaka Y., Matsuura T., Haga N., Mitsui Y.;

Toole 264:153-161(2001).

B MBL, AB035309; BAB1887.1; --

R InterPro; IPR000477; RVTse.

R InterPro; IPR000345; Telomerase_RT.

P Fam; PF0078; Yrt; 2.

P Fam; PF0078; Yrt; 2.

R RNA-directed DNA polymerase; Transferase.

SEQUENCE 895 AA; 107086 MW; 130C0DB32FD11C76 CRC64;
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Paramecium caudatum.
Bukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
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48.1%; Score 63; DB 5; Length 896;
Best Local Similarity 45.5%; Pred. No. 0.23;
Matches 10; Conservative 5; Mismatches 7; Indele
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47.6%; Pred. No. 0.33;
tive 4; Mismatches 7; Indels
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Telomerase reverse transcriptase.
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Matches 10; Conservative
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Q9GRCS;
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Search completed: November 12, 2003, 19:50:44 Job time: 23.1101 secs

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Sequence 217, App Sequence 217, App Sequence 217, App Sequence 21, Appl Sequence 21, Appl Sequence 225, App Sequence 25, Appl Sequence 25, Appl Sequence 225, Appl

Seguence 2, Appli Seguence 323, App

Sequence

Sequence 225, Sequence 225, Sequence 2, A

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Sequence

Sequence Sequence Sequence

Sequence:

Run on:

Searched:

Database

Result

Sequence 2 Sequence 1 Sequence 8

Sequence Sequence

Sequence Sequence Sequence

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APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chaman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020164786A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Two Embarcadero Center, 8th Floor
STREET: Two Embarcadero Center, 8th Floor
STREET: Two Embarcadero Center, 8th Floor
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER: EMADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IM PC compatible
COMPUTER: STATE: PLOPPY disk
COMPUTER: STATE: PLOPPY disk
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 26-APR-2001
CLASSIFICATION: 536
CURRENT APPLICATION: 536
                                      US-10-282-960-3

US-10-294-778-2

US-10-282-960-81

US-10-282-960-81

US-10-044-692-317

US-10-044-692-317

US-10-044-692-5

US-10-044-692-5

US-10-044-692-5

US-10-044-692-5

US-10-044-692-5

US-10-044-692-5

US-10-044-692-5

US-10-054-612-217

US-10-054-217-217

US-10-054-611-217

US-09-990-080-2

US-09-991-052-2

US-10-054-611-217

US-09-951-052-2

US-10-053-758-215

US-10-054-611-225

US-10-053-758-225

US-10-053-758-225

US-10-053-758-225

US-10-053-758-225

US-10-054-611-225
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APPLICATION NUMBER: US/08/654,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                      US-10-044-692-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
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Patent No. US20020164786A1
GENERAL INFORMATION:
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Sequence 115,
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

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          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-766-253-114
US-09-438-114
US-10-053-758-114
US-10-054-295-114
US-10-044-692-115
US-09-843-676-67
US-09-766-253-67
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1 ARTFRREKRAERLTSRVKALFSVLNYE 27
                                                                                                                                                                                                                                                                  644079 segs, 171749292 residues
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                           US-08-854-050-114
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Match Length
                                                                                                 November 12,
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Query Match
100.0%; Score 130; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e-13;
Matches 27; Conservative 0; Mismatches 0; Indels
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APPLICANT: Andrews, William H.
IIILE OF INVENTION: No. US20030009019A1el Telomerase
UNDER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
CLASSIFICATION S36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION S36
PRIOR APPLICATION S36
PRIOR APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION S36
PRIOR APPLICATION S36
PRIOR APPLICATION S36
PRIOR APPLICATION S36
PRIOR APPLICATION: 536
PRIOR APPLICATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California COUNTRY: United States of America ZIP: 9411-1884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION INFORMATION:
TELERPHONE: (415) 576-0200
                            TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 114:
                                                                                                                                                                                                                                                                                                      1 ARTFRREKRAERLTSRVKALFSVLNYE 27
                                                                                                                                                                                                                                                                                                                                                      1 ARTFREKRAERLTSRVKALFSVLNYE 27
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 114, Application US/09438486; Publication No. US20030009019A1
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
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NAME: Apple, Randolph T
REGISTRATION NUMBER: 36,
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LENGTH: 27 amino acids
TYPE: amino acid
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NAPPLICANT: CAPPLICANT: N
                                                                                                                      US-09-766-253-114
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COMPUTER: IBM PC compatible
OMPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PRILOGALICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION AUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US/09/764,643
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
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                                                   NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE TOWNER: 36,429
REPERENCE TOWNER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEFANE: (415) 576-0200
TELEFAN: (415) 576-0300
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 aming acids
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 130; DB 10;
Best Local Similarity 100.0%; Pred. No. 4.8e-13;
Matches 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: «Unknown»

TOPOLGGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-09-843-676-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ARTFREKRAERLTSRVKALFSVLNYE 27
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FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (415) 576-0300
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LENGTH: 27 amino acids
TYPE: amino acid
                                ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 114:
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                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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Andrews, William H.
TITLE OF INVENTION: No. US20030044953Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; DB 15;
4.8e-13;
hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/854,050
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
FILING DATE: 18-APR-1997
FILING DATE: 01-0CT-1996
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100.0%; Pred. No. 4.8
:ive 0; Mismatches
      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
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SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-10-054-295-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                      1 ARTFRREKRAERLTSRVKALFSVLNYE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ARTFREKRAERLTSRVKALFSVLNYE 27
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                                                                                                                                     RESULT 5
US-10-054-295-114
Sequence 114, Application US/10054295
Publication No. US20030044953A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,429
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CLASSIFICATION: 536
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Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPOLOGY: linear
      27; Conservative
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Best Local Similarity
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      Matches
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                                                                                     Length 27;
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COMPUTER: IPOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 13-Jan-2002
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING NUMBER: US 08/851,843
FILING NUMBER: US 08/851,843
                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                   , DB 11;
4.8e-13;
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Pred. No. 4.8e-13;
                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 4.8
Matches 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States of America ZIP: 94111
COMPUTER READABLE FORM:
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; SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-10-053-758-114
                                                                                                                                                                  1 ARTFRREKRAERLTSRVKALFSVLNYE 27
                                                                                                                                                                                          Sequence 114, Application US/10053758
Publication No. US20030032075A1
GENERAL INFORMATION:
APPLICANT: Ccth, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 576-0200
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100.0%;
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 California
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                 ; MOLECULE TYPE: peptide US-09-438-486-114
linear
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Best Local Similarity
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Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692
                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 130; DB 15; 100.0%; Pred. No. 4.8e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/912,951
FILING DATE: Unknown
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                     THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                            CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 115:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ARTFRREKRAERLTSRVKALFSVLNYE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 0. US-10-044-539-115; Application US/10044539; Sequence 115, Application US/10044539; Publication No. US20030100093A1; GENERAL INPORMATION:

Lingner, Joachim Nakamura, Toru Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 11-Jan-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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Harley, Calvin
Andrews, William H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: <Unknown>
Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ropology: linear
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Best Local Similarity 100.
Matches 27; Conservative
                                                                                                       SEQUENCES:
                                                                                                         NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-044-692-115
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                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IPOPPY disk
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRINT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                              Andrews, William H. TITLE OF INVENTION: No. US20030059787Alel Telomerase NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: 08/854,050
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
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100.0%; Pred. No. 4.8
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
COUNTRY: United States of America
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SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-10-054-611-114
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                  Sequence 114, Application US/10054611
Publication No. US20030059787A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 115, Application US/10044692
Publication No. US20030096344A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 576-0200
                                                                                APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 114: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.(
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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US-10-054-611-114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020187471Alel Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
            ADDRESSEE: Townsend and Townsend and Crew LLP
                               wo Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
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2.9e-12;
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FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
PILLING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY_AGENT INFORMATION:
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100.0%; Pred. No. 2.9
ive 0; Mismatches
                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
                                                                                                COUNTRY: United States of America
                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 ARTFRREKRAERLTSRVKALFSVLNYE 127
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(15) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 129 amino acids TYPE: amino acid
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Chapman, Karen B.
Morin, Gregg B.
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 576-
INFORMATION FOR SEQ ID NO: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                              COMPUTER READABLE FORM:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27; Conservative
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US-09-766-253-67
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TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
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                                                                                                                                                                                COUNTRY: United States of America
COUNTRY: United States of America
TIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002
CLASSIFICATION: 435
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TITLE OF INVENTION: No. US20020164786A1el Telomerase
                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 015389-002600US TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/912,951
FILING DATE: «UDARNOWN)
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAX-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MX-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 01-OCT-1996
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 115:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ARTFREKRAERLISRVKALFSVLNYE 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 67, Application US/09843676
Patent No. US20020164786A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 115
SEQUENCE CHARACTERISTICS:
                                                                                                                                          CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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Best Local Similarity 100.
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELEFAX: (415)
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Gaps

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12-NOV-1999
APPLICATION NUMBER:
                                             CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 130; DB 10; Length 129; Best Local Similarity 100.0%; Pred. No. 2.9e-12; Matches 27; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cech, Thomas R.
APPLICANT: Cech, Thomas R.
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US2003009019Alel Telomerase
NUMBER OF SEQUENCES: 223
APPLICANT: ADRESS:
                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: <UNKnown>
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
ATTORNEY/AGENT INFORMATION:
     COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 ARTFRREKRAERLTSRVKALFSVLNYE 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acids
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Peptide
LOCATION: 1..129
                              ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-438-486-67
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Length 129;
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Sequence 67, Application US/10053758

Publication No. US20030032075A1

GENERAL INFORMATION:
Lingner, Joachim:
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Galvin
Andrews, William H.

TITLE OF INVENTION:
NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1.129 / OTHER INFORMATION: /note= "TRT motifs from human" US-09-438-486-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 130; DB 11; 100.0%; Pred. No. 2.9e-12;
                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 2...
Matches 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 ARTFRREKRAERLTSRVKALFSVLNYE 127
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                   APPLICALL.

APPLICAL.

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,017

TITING DATE: 25-APR-1997
                                                                                                                            FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFFCATION: 536
                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Peptide LOCATION: 1..129
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OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Andrews, William H.
TITLE OF INVENTION: No. US20030059787A1el Telomerase NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 130; DB 15;
Best Local Similarity 100.0%; Pred. No. 2.9e-12;
Matches 27; Conservative 0; Mismatches 0;
                                                                                                                       FILING DATE: «UNKNOWN:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
              APPLICATION NUMBER: US/10/054,295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: California COUNTRY: United States of America
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FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 ARTFREKRAERLISRVKALFSVLNYE 127
                                                                                                      APPLICATION NUMBER: 08/854,050
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                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 67, Application US/10054611
Publication No. US20030059787A1
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Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 67
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94111
COMPUTER READABLE FORM:
                                                                                PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                      FILING DATE: 18-
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION
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APPLICANT Cech, Thomas R.
Linguer, Joachim
Nakamura, Toru
Chaman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030044953Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1.7129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
TWARE: Patentin Release #1.0, Version #1.30 APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Ploor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 130; DB 15; 100.0%; Pred. No. 2.9e-12;
                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/654,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/651,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/646,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States of America
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Publication No. US20030044953A1
GENERAL INFORMATION:
                                                                         FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 129 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94111
                             CURRENT
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Query Match
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Matches
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Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1.129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS: ADDRESSE: Townsend and Crew LLP
                                                                                                                                                                              NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/COCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 130; DB 15; 100.0%; Pred. No. 2.9e-12;
                 FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-AR-1997
APPLICATION NUMBER: US 08/84,419
FILING DATE: 18-ARR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 ARTFRREKRAERLISRVKALFSVLNYE 127
APPLICATION NUMBER: 08/854,050
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US-10-044-692-13
Sequence 13, Application US/10044692
Publication No. US20030096344A1
Bublication No. US2003009634A1
CENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: <Unknown>
                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-054-611-67
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: /note= "TRT motifs from human" US-10-044-692-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 130; DB 15; ilarity 100.0%; Pred. No. 2.9e-12; Conservative 0; Mismatches 0;
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: November 12, 2003, 19:55:47
Job time: 21.566 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ARTFRREKRAERLISRVKALFSVLNYE 27
                                                                                                                                                                                                                                                                              TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: <Unknown>TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 576-0:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 27; Conserva
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

November 12, 2003, 19:43:04; Search time 10.5283 Seconds (without alignments) 246.626 Million cell updates/sec Run on:

1 ARTFRREKRAERLTSRVKALFSVLNYE 27 US-08-854-050-114 130 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 seqs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

283308

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | æ | | | SUMMAKIES | |
|---------------|-------|-------|--------|-----|-----------|--------------------|
| Result No. | Score | Query | Length | DB | ID | Description |
| - | 130 | 100.0 | 1132 | . 2 | T03844 | telomerase catalvt |
| 7 | 51 | 39.5 | | ~ | B81120 | |
| m | 49 | 37.7 | e | N | T45089 | pyruvate synthase |
| 4 | | 37.7 | | ~ | JE0248 | ATP-binding casset |
| ß | 48 | 36.9 | m | 7 | F81030 | ABC transporter, p |
| 9 | 48 | 36.9 | | 7 | F81976 | a) |
| 7 | 48 | ė. | | N | F71114 | probable ferredoxi |
| 80 | 48 | 36.9 | | N | AH0315 | |
| о | 47.5 | | | 7 | 853900 | cal |
| 10 | 47 | Ψ | | N | T49535 | |
| 11 | 46 | 35.4 | 135 | 7 | D84730 | 60S ribosomal prot |
| 12 | 46 | 35.4 | | 7 | D69500 | |
| 13 | 46 | 35.4 | 462 | 7 | T25544 | hypothetical prote |
| 14 | 46 | 35.4 | 474 | - | IMBP4 | |
| 15 | 45 | 4. | 98 | 7 | A81902 | hypothetical prote |
| 16 | 45 | 34.6 | 321 | ~ | D90302 | μ |
| 17 | 45 | 4. | 334 | ~ | F75046 | pyruvate synthase |
| 18 | 45 | • | 436 | 7 | H97270 | |
| 19 | 44.5 | 34.2 | 335 | ~ | E96799 | probable carboxyph |
| 20 | 44 | 33.8 | 40 | 7 | C32338 | |
| 21 | 44 | ٠ | 159 | • | A70515 | probable bfrA prot |
| 22 | 44 | ٠ | | | MOCH2G | myosin regulatory |
| 23 | 44 | • | 172 | | I51690 | |
| 24 | 44 | ٠ | 172 | | B37100 | |
| 25 | 44 | ٠ | 172 | | A61034 | |
| 56 | 44 | ë. | 172 | ~ | A37100 | |
| 27 | 44 | 33.8 | 172 | 7 | S45709 | myosin regulatory |
| 28 | 44 | 33.8 | 172 | N | 152831 | myosin regulatory |
| 53 | 44 | 33.8 | 172 | ~ | T20273 | hypothetical prote |

| heat shock protein | heat shock protein | myosin regulatory | histidyl-tRNA synt | protein C46E10.3 (| recombination prot | probable nodulatio | excinuclease ABC c | groovin gene prote | T-cell receptor al | hypothetical prote | T-cell receptor al | T-cell receptor al | hypothetical prote | probable bacteriof | myosin regulatory |
|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|
| C64584 | E71929 | S11632 | C45734 | E88108 | F70350 | H71069 | B71893 | T13734 | 803525 | H71204 | S22899 | S21918 | B72230 | T35494 | A39932 |
| 7 | 0 | 7 | 7 | ~ | 7 | 7 | 7 | ~ | ~ | N | ~ | ~ | 7 | 7 | ~ |
| 80 | 180 | 189 | 328 | 392 | 520 | 534 | 594 | 4151 | 66 | 104 | 111 | 118 | 128 | 167 | 174 |
| _ | | | | | | | | | | | | | | | |
| | 33.8 | 33.8 | 33.8 | 33.8 | 33.8 | 33.8 | 33.8 | 33.8 | 33.1 | 33.1 | 33.1 | 33.1 | 33.1 | 33.1 | 33.1 |
| | 44 33.8 | 44 33.8 | 44 33.8 | 44 33.8 | 44 33.8 | 44 33.8 | 44 33.8 | 44 33.8 | 43 33.1 | 43 33.1 | 43 33.1 | 43 33.1 | 43 33.1 | 43 33.1 | 43 33.1 |

ALIGNMENTS

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Approximate range (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C; Accession: TM: Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J Soience 277, 955-959, 1997
A; Title: Telomerase catalytic subunit homologs from fission yeast and human.
A; Reference number: Z15111; MUID:97400623; PMID:9252327
A; Accession: T03844
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; tra
telomerase catalytic chain - human
N;Alternate names: telomerase reverse transcriptase
```

Gaps ö Query Match 100.0%; Score 130; DB 2; Length 1132; Best Local Similarity 100.0%; Pred. No. 1.8e-11; Matches 27; Conservative 0; Mismatches 0; Indels 0;

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RESULT 2
B91120
hypothetical protein NMB1120 [imported] - Neisseria meningitidis (strain MC58 serogroup C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: B81120
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: B81120
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: B8120
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: B8120
A;Authors: Grandi, G; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUD:20175755; PMID:10710307
A;Status: preliminary
A;Residues: 1-98 <TET>
A;Cross-references: GB:AE002461; GB:AE002098; NID:97226350; PIDN:AAF41510.1; PID:972263
C;Genetics:
A;Gene: NMB1120

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C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: F81030
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Pleischmann, R.D.; Dougherty, B.A. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V. A;Atlitle: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Accession: F91030
                                                                                                                                                                                                                                                                                                                                                                         A Status: preliminary
A Molecule type: DNA
A Molecule type: 1-121 «TET»
A Cross-references: GB:AE002538; GB:AE002098; NID:g7227136; PIDN:AAF42214.1; PID:g72271
A Experimental source: serogroup B, strain MC58
A Genetics:
A Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable ferric enterobactin transporter binding protein NMA0577 [imported] - Neisseria C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
R;Parkhili, 0;Accession: F81976
Holroyd, S;Jagels, K;Leather, S;Moule, S;Mungall, K;Quail, M.A.; Rajandream Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A;Accession: F81976
A;Accession: F81976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-321 cPRA.
A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CABB3868.1; PID:g73793
A;Experimental source: serogroup A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Date: 10-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
R;Accession: F71114
M; Ohfuku, Y; Suwada, M; Horikawa, H; Haikawa, Y; Hino, Y; Yamazaki, J; Kushida, N; Oguch M; Ohfuku, Y; Funahashi, T; Tanaka, T; Kudoh, Y; Yamazaki, J; Kushida, N; Oguch A; Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A; Reference number: A71000; MUID:98344137; PMID:9679194
periplasmic solute-binding protein, probable NMB1880 [imported] - Neis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Accession: F71114
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Residues: 1-334 «KAM»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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(3
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14;
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36.9%; Score 48; DB

Best Local Similarity 45.5%; Pred. No. 14;

Matches 10; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || | :| || | ::: |||:
155 ARIFGKEARAAELKAQIDALFA 176
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45.5%;
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Best Local Similarity 45.5's
Matches. 10; Conservative
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A;Gene: fetB2; NMA0577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
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C;Keywords: coenzyme A; oxidoreductase
F;2-311/Product: 2-oxisovalerate-ferredoxin oxidoreductase beta chain #status experimen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Date: 05-Dec-1270 ......
C; Accession: JE0248
R; Hirsch-Ernst, K.I.; Gaini-Rahimi, S.; Ernst, B.P.; Schmitz-0000-1.
Biochem. Biophys. Res. Commun. 249, 151-155, 1998
A; Title: Molecular cDNA cloning and tissue distribution of mRNA encoding a novel ATP-bin A; Reference number: JE0248; MUID: 98381042; PMID: 9705847
A; Accession: JE0248
A; Accession: JE0248
A; Accession: JE0248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RiKletzin, A.; Adams, M.W.
J. Bacteriol. 178, 248-257, 1996
A;Title: Molecular and phylogenetic characterization of pyruvate and 2-ketoisovalerate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Cross-references: GB:AJ003004; NID:g2970020; PIDN:CAA05793.1; PID:g2982567; Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology; Keywords: ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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A;Amolecule type: DNA
A;Rosidues: 1-331 **CKLE>
A;Cross-references: EMBL: K85250; NID:g1197352; PIDN:CAA59506.1; PID:g1197364
A;Experimental source: DSM 3638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP-binding cassette half-transporter - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                pyruvate synthase (EC 1.2.7.1) beta chain (validated) - Pyrococcus furiosus C;Species: Pyrococcus furiosus C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 03-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 27;
7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Complex: homotetramer of alpha, beta, delta, and gamma chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 331;
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   Length 98
                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: Z22908; MUID: 96125254; PMID: 8550425
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A;Residues: 1-836 <HIR>
A;Cross-references: GB:AJ003004; NID:g2970020; PIDN:CP
C;Superfamily: unassigned ATP-binding cassette proteir
C;Keywords: ATP
F;606-800/Domain: ATP-binding cassette homology <ABC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
10;
      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Mismatches
                                                                   10; Mismatches
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Pred. No.
   39.2%; Score 51; 36.0%; Pred. No.
                                                                                                                                1 ARTFRREKRAERLTSRVKALFSVLN 25
                                                                                                                                                                      SRTYRRARLAQKPKTRWKILYTLIN 60
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FRRDMNTQENATRARAVDSLLNFE 461
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illarity 37.5%;
Conservative 7
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Best Local Similarity 41.7%;
Matches 10; Conservative
                                                                      Conservative
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Best Local Similarity
Matches 9; Conserv
   Query Match
Best Local Similarity
Matches 9; Conserv
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RESULT 5 \$81030

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A,Map position: 2
C,Superfamily: rat ribosomal protein L27
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48.1%;
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A;Accession: T49535
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-617 <SCH>
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Best Local Similarity
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Matches
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R.Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. R.Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. and-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, A.Title: Genome sequence of Yersinia postis, the causative agent of plague.

A.Accession: AH0315

A.Accession: AH0316
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R; Poehlmann, R.; Philippsen, P.
Yeast 12, 391-402, 1996
A; Title: Sequencing a cosmid clone of Saccharomyces cerevisiae chromosome XIV reveals 12 A; Reference number: S63925; MUID: 96267764; PMID: 8701611
A;Cross-references: GB:AP000003; NID:g1236130; PIDN:BAA29776.1; PID:g3257093
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank C;Genetics:
A;Gene: PH0685
C;Superfamily: pyruvate synthase beta chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable ABC transport protein YPO2588 [imported] - Yersinia pestis (strain CO92) C;Species: Yersinia pestis C;Date: 02-Nov-2001 #text_change 17-May-2002
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C;Species: Saccharomyces cerevisiae
C;Species: Sasson: S53900; S63010; S63929
R;Poehlmann, R.; Philippsen, P.
Submitted to the EMBL Data Library, April 1995
A;Reference number: S53906
A;Reference number: S53906
A;Molecule type: DNA
A;References: EMBL:X66470; NID:g791101; PID:g791106
R;Poehlmann, R.; Philippsen, P.
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submitted to the Protein Sequence Database, April 1996
A;Reference number: S62997
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Best Local Similarity 37.5%; Pred. No. 15;
Matches 9; Conservative 7; Mismatches
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Best Local Similarity
Matches 10; Conserv
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A; Residues: 1-407 < POW>
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A,Map position: 6
A;Introns: 42/1; 222/3; 292/2
C;Superfamily: 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase homo F;169-300/Domain: 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase hr
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C;Species: Neurospora crassa
C;Date: O2-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 28-Jul-2000
C;Accession: T49935
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu submitted to the Protein Sequence Database, May 2000
                                                                                                                                                                                  PIDN:CAA60180.1; PID:g791106
to the EMBL Data Library, April 1995
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Afiltle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84730
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A;Molecule type: DNA
A;Residues: 1-135 <STO>
A;Cross-references: GB:AE002093; NID:g4263697; PIDN:AAD15383.1; GSPDB:GN00139
C;Genetics:
A;Gene: Atg32220
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A;Experimental source: BAC clone B21J21; strain OR74A
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 407;
A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-477 < POF> A;Cross-references: EMBL:X86470; NID:g791101; PIDN:CAA60180.1; PI A;Note: the nucleotide sequence was submitted to the EMBL Data Lic G;Genetics: A;Gene: SGD:JIP1 A;Cross-references: SGD:S0005022 A;Amap position: 14L A;Note: YNLO79w
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Pred. No. 22;
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Matches

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hypothetical protein NWA1329 [imported] - Neisseria meningitidis (strain 22491 serogrou C; Species: Neisseria meningitidis (c; Species: Neisseria meningitidis (c; Species: Neisseria meningitidis (c; Species: Os-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 (c; A2000 #sequence_revision 05-May-2000 #sperkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; More R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; More J.Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Altitle: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491. A; Reference number: A81775; MUID: 20222556; PMID: 10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GB:ALL57959; NID:g7379742; PIDN:CAB84580.1; PID:g738000
A, strain Z2491
                                                                                                                                                                                                                                                                                                                         A)Residues: 1-474 <KOB>
A)Cross-references: EMBL:AB016282; PIDN:BAA36658.1
A)Cross-references: EMBL:AB016282; PIDN:BAA36658.1
R;Cully, D.F.; Garro, A.J.
Gene 38, 153-164, 1985
A;Title: Nucleotide sequence of the immunity region of Bacillus subtilis bacteriophage
A;Reference number: A91535; MUID:86056972; PMID:3934047
C;Species: Bacillus phage phi-105
C;Date: 31-Dec-1988 #sequence revision 22-Oct-1999 #text_change 16-Jun-2000
C;Accession: T13541; C24521; D24521; E24521; F24521
R;Kobayashi, K.; Okamura, K.; Inoue, T.; Sato, T.; Kobayashi, Y.
submitted to the EMBL Data Library, July 1998
A;Bescription: Complete nucleotide sequence of Bacillus subtilis phage phi-105.
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A;Residues: 1-78, MTHC' < CUL>
A;Residues: 1-78, MTHC' < CUL>
A;Cross-references: GB:M11920; NID:g215477; PIDN:AAA88399.1; PID:g1196717
A;Accession: D24521
A;Accession: D24521
A;Molecule type: DNA
A;Residues: 149-160, AR', 163, 'H', 'HSDSQRRVR', 381-383, 'RIORRARS', 392 < CU2>
A;Cross-references: GB:M11920; NID:g215477; PIDN:AAA88401.1; PID:g1196719
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A;Residues: 'MP',119-376,'RNTK',381,'PGPWS' <CU4>
A;Cross-references: GB:M11920
C;Superfamily: phage phi-105 site-specific recombinase
C;Superfamily: phage phi-105
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
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Pred. No. 43;
5; Mismatches
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Similarity 50.0%;
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A;Experimental source: serogroup
C;Genetics:
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A;Residues: 189-318, 'HAP' <CU3>
A;Cross-references: GB:M11920
A;Accession: F24521
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A;Molecule type: DNA
A;Residues: 1-98 <PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE000964; GB:AE000782; NID:g2689287; PIDN:AAB89249.1; PID:g264853
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A;Cross-references: EMBL:U97592; PIDN:AAB52870.1; GSPDB:GN00028; CESP:C14A11.3
A;Experimental source: strain Bristol N2; clone C14A11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T25544
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submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid C14All.
                                                             DB 2;
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58.8%; Pred. No. 18;
tive 4; Mismatches
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A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
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A;Map position: X
A;Introns: 38/3; 73/3; 153/2; 325/3; 440/3
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A; Residues: 1-200 <KLE>
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A Londono-Vallejo J.A.;

I Sequence of a BAC carrying the entire hTERT gene.";

Submitted (OCT-2001) to the EMBL/GenBank/DBBJ databases.

Submitted (OCT-2001) to the EMBL/GenBank/DBBJ databases.

THE REPLICATION OF CHROMOSOME TERMINI IN MOST BUKARYOTES. IT

ELONGATES TELOMERASE IS A RIBONUCLEOPROTETH ENYME ESSENTIAL FOR THE REPLICATION OF CHROMOSOME ENDS BY COPYING A TEMPLE SEQUENCE MITHIN THE RNA COMPONENT OF THE ENZYME.

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SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.

SUBGRILULAR LOCATION: Nuclear.

-!- SUBGRILLIANION AND CANCER CELL PATHOGENESIS.

-!- IMMORTALIZATION AND CANCER CELL PATHOGENESIS.

-!- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
                                                                                                                                                                                    schizosacch
                                                                                                                                    rickettsia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=97433088; PubMed=9288757;
Meyerson M., Counter C.M., Eaton E.N., Ellisen L.W., Steiner P.,
Caddie S.D., Ziaugra L., Beijersbergen R.L., Davidoff M.J., Liu Q.,
Bacchetti S., Haber D.A., Weinberg R.A.;
"HESTZ, the putative human telomerase catalytic subunit gene, is up-
regulated in tumor cells and during immortalization.";
                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99267414; PubMed=1033526; Wick M., Zubov D., Hagen G.; "Genomic organization and promoter characterization of the gene encoding the human telomerase reverse transcriptase (HTERT).";
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09nxw2
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0043869
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P12258
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P52658
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                                            RECF XYLFA
DJBC HUMAN
APA4 HUMAN
PLSB SPIOL
YSR2 CAEEL
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MEDLINE-97400623; PubMed-9252327;
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014746; 014783;
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(c) 1993 - 2003 Compugen Ltd.
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1 YEAST
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length: 2000000000
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Score

Result 8 47.5

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Minimum DB seq Maximum DB seq

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Sequence:

Scoring table:

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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                          GO; GO:0005696; C:telomere; TAS.
GO; GO:000721; F:telomeric template RNA reverse transcriptas. . .; TAS.
GO; GO:0007003; P:telomere binding; TAS.
InterPro; IPR00477; RVTse.
InterPro; IPR003545; Telomerase_RT.
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PRINTS; PR01365; TELOMERASERT.
Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Telomerase catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drissi R., Cleveland J.L.;

Partial sequence of Mus musculus telomerase catalytic subunit homolog.";

Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: TELOMERASE IS A RIBONUCLEDSFOTEIN ENZYME ESSENTIAL. IT HE REPLICATION OF CHROWOSCHE TERMINI IN MOST BUKARYOTES. IT BLONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Greenberg R.A., Allsopp R.C., Chin L., Morin G.B., DePinho R.A., "Expression of mouse telomerase reverse transcriptase during development, differentiation and proliferation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98393668; PubMed-9724727;
Martin-Rivera L., Herrera E., Albar J.P., Blasco M.A.;
"Expression of mouse telomerase catalytic subunit in embryos and
                                                                                                                                                                                                                                                                                                                                                                            ;
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1132 AA; 126996 MW; 94E35469C4CA33A0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.0%; Pred. No. 9.1e-12; Matches 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TERT_MOUSE STANDARD; PRT; 1122 AA. 070372; 035432; 30-May-2000 (Rel. 39, Created) S. May-2000 (Rel. 39, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Telomerase reverse transcriptase (EC 2.7.7.-)
                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 130;
                                                                                                                                                                                                                                                                                                                                                                                                                            642 ARTFRREKRAERLTSRVKALFSVLNYE 668
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                                                                                    EMBL, AF015950; AAC51672.1; --
EMBL, AF128991, AAC51724.1; --
EMBL, AF128993, AAD3037.1; --
EMBL, AF128993, AAD30037.1; --
EMBL, AX007685; AAG23289.1; --
GENEW, HGNC.11730; TERT.
MIM, 187270; --
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pyruvate synthase subunit porB (EC 1.2.7.1) (Pyruvate oxidoreductase beta chain) (POR) (Pyruvic-ferredoxin oxidoreductase bocs or PF0965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
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STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
MEDLINE=96125254; PubMed=8850425;
MEDLINE=96125254; PubMed=8850425;
"Kletain A., Adams M.W.W."
"Molecular and phylogenetic characterization of pyruvate and 2-ketoisovalerate ferredoxin oxidoreductases from Pyrococcus furiosus and pyruvate ferredoxin oxidoreductase from Thermotoga maritima.";
J. Bacteriol. 178:248-257(1996).
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MEDLINE=93136227; PubMed=8380721;
Blamey J.M., Adams M.W.W.;
"Purification and characterization of pyruvate ferredoxin exidoreductase from the hyperthermophilic archaeon Pyrococcus
                                                           SUBUNIT: Interacts with PINXI (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
TELOMERASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
Weise R.B., Dunn D.M., Robb P.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 73; DB 1; Length 1122;
Pred. No. 0.0041;
4; Mismatches 8; Indels
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127977 MW; F85266905DD6558C CRC64;
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InterPro; IPR003545; Telomerase_RT.
Pfam; PF00078; rvt; 1.
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l Similarity 53.8%;
14; Conservative .
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1122 AA;
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Best Local Similarity
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NCBI_TaxID=2261;
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                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                   ö
furiosus.";
Biochim. Biophys. Acta 1161:19-27(1993).
-!- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
COA + CO(2) + reduced ferredoxin.
-!- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Oteuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Robb F.T., Horikoshi K.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Msuchi Y., Shizuya H., Kikuchi H.,
Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.",
DNA Res. 5:55-76(1998).
-!- CATALYIIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
COA + CO(2) + reduced ferredoxin.
-!- SUBUNIT: HETEROTERAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE
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058417:
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
Pyruvate synthase subunit porB (EC 1.2.7.1) (Pyruvate oxidoreductase
heta chain) (POR) (Pyruvic-ferredoxin oxidoreductase beta subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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                                                                                                                                                                                                                                                        Oxidoreductase; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=S288c / FY1679;
MEDLINE=96267764; PubMed=8701611;
Pochlmann R., Philippen P.;
"Sequencing a cosmid clone of Saccharomyces cerevisiae chromosome XIV reveils 12 new open reading frames (ORFs) and an ancient duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABC6_HUMAN STANDARD, PRT; 842 AA.
Q9NP58; 075542;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
ATP-binding cassette, sub-family B, member 6, mitochondrial precursor (Mitochondrial ABC transporter 3) (Mt-ABC transporter umat).
ABCB6 OR MTABC3.
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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m
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Hypothetical 45.9 kDa protein in TPM1-MKS1 intergenic region.
YNLO78W OR N2337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 407;
                                                                             Score 48; DB 1; Length 330;
                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                      330 AA; 35987 MW; 1F3598D66BF2C6FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 407 AA; 45908 MW; 925C7B6063BCE4F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.5%; Score 47.5; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGD; S0005022; JIP1.
GO; GO:0005935; C:bud neck; IDA.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:0007088; P:regulation of mitosis; IPI.
                                                                                                                                                                                                                                                                                                                                                                                       407 AA
                                                                                                          Pred. No. 7; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIRREDRQAKVRSRFRSKKELTSVLNY 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                         299 FKRPEAIEELRNQIKAMWKVLGVE 322
                                                                                                                                                                                          4 FRREKRAERLTSRVKALFSVLNYE 27
                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                             36.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X86470; CAA60180.1; -. EMBL; Z71354; CAA5952.1; -. PIR; S53900; S53900. SGD; S0005022; JIP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.18;
                                                                                                          Local Similarity 37.5
nes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of six ORFs.
                                                                                                                                                                                                                                                                                                                                                                                 YNH8 YEAST
P53939;
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                                                                                                                                                                                                                                                                                                                                                                                                      A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rtausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Riansner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Batcow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Batcow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Brownstely R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Madan A., Young A.C., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
M. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
                                                                                            SEQUENCE FROM N.A.
MEDIJIRE_2029824; PubMed=10837493;
MILSIJIRE_20298824; Nulki T., Senbongi H., Yokoi N., Yano H., Miyazaki M.,
Mitsuhashi N., Miki T., Senbongi H., Yokoi N., Yano H., Miyazaki M.,
Nakajima N., Iwanaga T., Yokoyama Y., Shibata T., Seino S.;
"MTABG3, a novel mitochondrial ATP-binding cassette protein involved J. in iron homeostasis.";
J. Biol. Chem. 275:17536-17540(2000).
                                                                                                                                                                                                                                                                     Hirsch-Ernst K.I., Schaefer A., Ernst B.P., Schmitz-Salue Awuah D., Kahl G.F., "Subcellular localization of the ABC transporter umat."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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EMBL, AB039354; BAA96733.1; JOINED.
EMBL, AB039355; BAA96733.1; JOINED.
EMBL, AB039356; BAA96733.1; JOINED.
EMBL, AB039357; BAA96733.1; JOINED.
EMBL, AB039589; BAA96733.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human and mouse cDNA sequences.
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EMBL: AF076775; AAF75107.1; -.
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EMBL; AB039357; BAA96733.1;
EMBL; AB039358; BAA96733.1;
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Homo sapiens (Human)
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
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                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
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Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O., Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C., Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.; "An integrated analysis of the genome of the hyperthermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyrococcus abyssi.
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00211; ABC TRANSPORTER 1; 1.
PROSITE; PS50893; ABC TRANSPORTER 2; 1.
ATP-binding; Transmembrane; Transport; Mitochondrion; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Pyruvate synthase subunit panB (EC 1.2.7.1) (Pyruvate oxidoreductase
beta chain) (POR) (Pyruvic-ferredoxin oxidoreductase beta subunit).
PORB OR PYRAB13620 OR PAB1476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E63A7D59DCE5B9ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MITOCHONDRION (POTENTIAL)
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Pred. No. 38;
6; Mismatches
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InterPro; IRR001140; ABC TW transpt.
InterPro; IPR001409; ABC Transporter.
Pfam; PF000664; ABC_membrane; 1.
Pfam; PF00005; ABC_tran; 1.
Propon; PD000006; ABC_tran; 1.
SMO0182; AAA; 1.
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                  JOINED.
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JOINED.
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                                                  , AB003362; BAA96733.1; JOI
, AB003363; BAA96733.1; JOI
, AB039364; BAA96733.1; JO
L; AB033365; BAA96733.1; JC
L; AB03366; BAA96733.1; JC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 35.4%;
Best Local Similarity 37.5%;
Matches 9; Conservative
                                                                                                                                                                                                                                                              EMBL; BC000559; AAH00559.1;
EMBL; AF070598; AAC28653.1;
HSSP; P13569; 1NBD.
Genew; HGNC:47; ABCB6.
                    BAA96733.1;
BAA96733.1;
                                                                                                                                                                         BAA96733.1;
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BAA96733.1;
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NCBI_TaxID=29292;
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PubMed=12622808;
AB039359;
AB039360;
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1148
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                                             AB039361;
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TRANSIT
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Q9UYZS;
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NP BIND
SEQUENCE
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EMBL;
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                                                                                                                                                                         EMBL;
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5 RREKRAERLISRVKALFSVL 24
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28-FEB-2003 (Rel. 41, Last seq
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                                   4 REEVRASRPTKEMKMIFDVL
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                                                                                                                                                                                                                                                                                        Clostridium acetobutylicum.
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HAMAP; MF 00089; -; 1.
InterPro; IPR002817; ThiC.
                                                                                                                                                STANDARD;
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097EU2;
                                                                                                                     049290
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                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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archaeon Pyrococcus abyssi.";
Mol. Microbiol. 47:1495-1512(2003).
-!- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
                                                         CoA + CO(2) + reduced ferredoxin.
-!- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WEDLINE=88058763; PubMed=1680169; Utatsu I., Sakamoto S., Imura T., Toh-E A.; Utatsu I., Sakamoto S., Imura T., Toh-E A.; "Yeast plasmids resembling 2 micron DNA: regional similarities and diversities at the molecular level."; J. Bacteriol. 169:5537-5545(1987).
J. Bacteriol. 169:5537-5545(1987).
J. PUNCTION: PLASMID PARTITION REQUIRE REP1, REP2, AND A CIS-ACTING DNA SEQUENCE (KNOWN AS STB). REP 1 MAY ACT BY INTERCALATING IN THE YEAST NUCLEAR MATRIX AND BINDING STB EITHER DIRECTLY OR VIA
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.
NCBI_TaxID=4954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
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0
                                                                                                                                                                                                                                                                                                                                                                                                     34.6%; Score 45; DB 1; Length 330; 33.3%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.6%; Score 45; DB 1; Length 357; 50.0%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
                                                                                                                                                                                                                                                                                                                                                              330 AA; 36065 MW; 50428984BD5D9D99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40752 MW; 7DF4C06359D4BA35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -! - SIMILARITY: TO THE P GENE PRODUCT OF PSR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN'1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-JAUG-1990 (Rel. 15, Last annotation update)
Trans-acting factor B (REP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357 AA.
                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                  EMBL; AJ248287; CAB50267.1; ALT INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 FKRPEAIDELRNQIKAMWKVLGVE 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 FRREKRAERLISRVKALFSVLNYE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M18274; AAA35283.1; -. Plasmid; Trans-acting factor. SEQUENCE 357 AA; 40752 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 33.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zygosaccharomyces bailii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 50.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=IFO 1047;
                                                                                                    GAMMA CHAIN
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P13776;
                                                                                                                                                                                                                                                                                                                                         INIT MET
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.M., Koonin E.V., Smith D.R., "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.", J. Bacteriol. 183:4823-4838(2001).

J. Bacteriol. 183:4823-4838(2001).

HMP) moiety of thiamine (4-amino-2-methyl-5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Jo-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative carboxyvinyl-carboxyphosphonate phosphorylmutase
FEC 2.7 3.33) (Carboxyphosphonoenolpyruvate phosphonomutase)
Phosphonomutase)
ATIG77060 OR FE28C20.14.
                                                                                                                                                                                                                                     Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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TIGRFAMS; TIGR00190; thic; 1.
Thiamine biosynthesis; Complete proteome.
SEQUENCE 436 AA; 48495 MW; 60DE4DD890C92737 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.6%; Score 45; DB 1; 56.2%; Pred. No. 27;
                                                                                                                    Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (By similarity)
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436 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PATHWAY: Thiamine biosynthesis.
                                                                                    Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
                                                                              28-FEB-2003 (Rel. 41, Last sequence
28-FEB-2003 (Rel. 41, Last annotati
Thiamine biosynthesis protein thic.
THIC OR CAC3014.
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Harris D.

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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Whole genome comparison of Mycobacterium tuberculosis clinical and
                                      MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Esglmeier K., Gas S., Bary C.E. III, Tekaia F., Badcock K., Bashma D., Brown D., Chillingworth T., Connor R., Davies R., Devin M., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.B., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z97193; CAB10050.1; -. EMBL; AE007049; AAK46197.1; PPIR; A70515; A70515.
                                                                                                                                                                                                                                                                               complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CDC 1551 / Oshkosh; Fleischmann R.D., Alland D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tuberculist; Rv1876; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
9; Conserve
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P39416; P39417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YOOF BPT4
ID _YOOF_BPT4
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g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
                                                                                                                                                    STRAIN=CV. Columbia;

MEDLINE=21016719; PubMed=11130712;

MEDLINE=21016719; PubMed=11130712;

MEDLINE=21016719; PubMed=11130712;

MURICE O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

White O., Alonso J., Altafi H., Cheuk R.F., Chin C.W.,

Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Fordsy T.H., Dowar K.,

A Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B.,

Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.W., Lanz C.A., Li J.H., Li Y.-P.,

Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Militscher J., Miranda M., Nguyen M., Neoney T., Rowley D.,

Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Pai G., Peterson J., Tambunga G., Toriumi M.J., Town C.D.,

Nu D., Yu G., Fraser C.M., Verter J.C., Davis R.W.;

"Left Charack T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

"Left C. M., Van Aken S., Vaysberg M., South Arabidopsis

"Left C. M., Van Aken S., Vaysberg M., South Arabidopsis
                                             core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 408:816-820(2000).
-!- CATALYTIC ACTIVITY: 1-carboxyvinyl carboxyphosphonate = 3-(hydrohydroxyphosphoryl)pyruvate + CO(2).
-!- SIMILARITY: BELONGS TO THE ISOCITRATE LYASE FAMILY. CPEP MUTASE
                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosid
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335 AA; 36103 MW; 4390671598ADA83B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 34, Last annotation update)
Bacterioferritin (BFR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.2%; Score 44.5; Di
50.0%; Pred. No. 24;
ive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacterioterritin (BFK).
BFR OR RV1876 OR MT1925 OR MTCY180.42C.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD001857; Isocit_lyase_ph; 1.
PROSITE; PS00161; ISOCITRATE_LYASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; E96799; E96799.
InterPro; IPR000918; Isocit_lyase_ph.
Pfam; PF00463; ICL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 TFRREKRAERL---TSRVKALF 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 TFRRNPRAARLVNPTARIQTRF 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AC002291; AAC00621.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                      SEQUENCE FROM N.A.
                                                                                      NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thaliana."
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008465;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRON (HEME AXIAL LIGAND) (POTENTIAL) 098B6D7392A9CD60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.8%; Score 44; DB 1; Length 159; 33.3%; Pred. No. 13; ive 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Iron storage, Heme, Complete proteome.
DOMAIN 1 145 FERRITIN-LIKE DIIRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ź
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ARTFRREKRAERLTSRVKALFSVLNYE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002024; Bacterioferritin.
InterPro; IPR001519; Perritin.
Pfam; PP00210; ferritin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00601; BACFERRITIN.
ProDom; PD002269; Bacterioferritin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGREAMS, TIGR00754; bfr; 1.
PROSITE, PS00549; BACTERIOFERRITIN; 1.
PROSITE, PS50905; FERRITIN_LIKE; 1.
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[1]
SEQUENCE FROM N.A.
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MLRB_RAT
ID MLRB_RAT
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SEQUENCE
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MOD RES
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                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Fischer;
MEDLINE=90361739; PubMed=2391362;
Grant J.W., Taubmann M.B., Church S.L., Johnson R.L., Nadal-Ginard B.;
Grant J.W., Taubmann M.B., Church S.L., Johnson R.L., Nadal-Ginard B.;
"Mammalian nonsarcomeric myosin regulatory light chains are encoded
by two differentially regulated and linked genes.";
J. Cell Biol. 111:1127-1135(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taubman M.B., Grant J.W., Nadal-Ginard B., "Cloning and characterization of mammalian myosin regulatory light chain (RLC) cDNA: the RLC gene is expressed in smooth, sarcomeric,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0AN-1990 (Rel. 13, Created)
01-0AN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Myosin regulatory light chain 2-A, smooth muscle isoform (Myosin
                                                                          Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical 19.7 kDa protein in motB-dexA intergenic region.
YOOF OR MOTB.2 OR DEXA.-1.
                                                                                                                          SEQUENCE FROM N.A.
Uzan M., Spicer E., White T., Kutter E.M.;
"Two new orfs between dexA and motB in bacteriophage T4.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                    33.8%; Score 44; DB 1; Length 166;
                                                                                                                                                                                                     Kutter E., Arisaka F., Kunisawa T., Tsugita A., Mosig G., Mesyaazhinov V., Ruger W., Stidham T., Thomas E.; "Bacteriophage T4 genome analysis."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                           Hypochetical protein.
SEQUENCE 166 AA; 19735 MW; 01CF5025E69A0E86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell Biol. 104:1505-1513(1987).
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MEDLINE=87222590; Pubmed=3584239;
                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF158101; AAD42611.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.78;
                                                                                                                                                                                                                                                                                                                                                                     EMBL; U76613; AAB26982.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 66.7
tes 8; Conservative
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5.RVESSFSILNYE 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and nonmuscle tissues.
                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                   NCBI_TaxID=10665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                               Bacteriophage T4
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P13832;
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Matches
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MLRA RAT
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Myosin; Calcium-binding; Muscle protein; Phosphorylation; Acetylation;
PEDITRE=91304271; PubMed=1649372;
Feinstein D.L., Durand M., Milner R.J.;
Fracterization of myosin regulatory light chains in rat brain:
Fracterization of movel isoform.";
Fractization of movel isoform.";
Fractization Brain Res. 10:97-105(1991).
Fractization Plays AN IMPORTANT ROLE IN REGULATION OF BOTH SMOOTH MUSCLE AND NONMUSCLE CELL CONTRACTILE ACTIVITY
FRESENCE OF CALCIUM AND CALMODULIN INCREASES THE ACTIVATED MYOSIN ATPASE ACTIVITY AND THEREBY REGULATES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Myosin regulatory light chain 2-B, smooth muscle isoform (Myosin
                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: Myosin is an hexamer of 2 heavy chains and 4 light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                           -!- MISCELLANEOUS: THIS CHAIN BINDS CALCIUM.
-!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Indels
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PHOSPHORYLATION (BY MLCK)
(BY SIMILARITY).
PHOSPHORYLATION (BY MLCK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B292DCD189F6D016 CRC64;
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EF-HAND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ARTFRREKRAERLTSRVKALF 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 EF
19764 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002048; EF-hand.
Pfam; PF00036; efhand; 3.
ProDom; PD000012; EF-hand; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X05566; CAA29080.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X54616; CAB38864.1; -. EMBL; X54617; CAA38437.1; -. PIR; A37100; A37100. HSSP; P13543; 1SCM.
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                                                                                                                                                                                                                                                                                                                     CONTRACTILE ACTIVITY.
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Matches 10; Conservative
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INIT MET 0
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Search completed: November 12, 2003, 19:48:01
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Myosin; Calcium-binding; Muscle protein; Phosphorylation; Acetylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                    Grant J.W.;
Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PLAYS AN IMPORTANT ROLE IN REGULATION OF BOTH SMOOTH
MUSCLE AND NONMUSCLE CELL CONTRACTILE ACTIVITY.
-!- ENZYME REGULATION: PHOSPHORYLATION OF MLC-2 BY THE ENZYME MLC
KINASE IN THE PRESENCE OF CALCIUM AND CALMODULIN INCREASES THE
ACTIVIATED MYOSIN ATPASE ACTIVITY AND THEREBY REGULATES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
STRAIN=Sprague-Dawley, TISSUE=Brain, and Liver;
MEDLINE=90361739; PubMed=2391362;
Grant J.W., Taubman M.B., Church S.L., Johnson R., Nadal-Ginard B.;
"Mammalian nonsarcomeric myosin regulatory light chains are encoded by two differentially regulated and linked genes.";
J. Cell Biol. 111:1127-1135(1990).
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01-MAR-1992 (Rel. 21, Last sequence update)
01-MAR-1992 (Rel. 41, Last annotation update)
Myosin regulatory light chain 2, smooth muscle minor isoform (G1)
(DINB) (MLC-2) (Isoform L20-B1).
                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: Myosin is an hexamer of 2 heavy chains and 4 light
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PHOSPHORYLATION (BY MLCK)
(BY SIMILARITY).
PHOSPHORYLATION (BY MLCK)
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Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                  -!- MISCELLANEOUS: THIS CHAIN BINDS CALCIUM.
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; Mismatches
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InterPro; IPR020484; EF-hand.
Pfam, PF00036; efhand; 3.
ProDom; PD000012; EF-hand; 2.
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Matches 10; Conservative
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18
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SĒQUENCE FROM N.A.
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INIT MET 0
MOD RES 1
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SEQUENCE
                                                                                                                                                                 REVISIONS
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                                                                                                                                          [2]
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00054; EFh; 2.
PROSITE; PS00018; EF HAND; 1.
Myosin; Calcium-binding; Muscle protein; Phosphorykation; Acetylation;
                                                                                 chicken gizzard.";
-1. **Lochem. 183:645-651(1989).

**Eur.** J. **BACCHEM.**
-1. **FUNCTION: PLASY AN IMPORTANT ROLE IN REGULATION OF BOTH SMOOTH MUSCLE AND NONMUSCLE CELL CONTRACTILE ACTIVITY.
-1. **EULAMTION: PHOSPHORYLATION OF MIC.2 BY THE BNZYME MLC KINASE IN THE PRESENCE OF CALCIUM AND CALMODULIN INCREASES THE KINASE IN THE PRESENCE OF CALCIUM AND CALMODULIN INCREASES THE ACTIN-ACTIVATED MYOSIN ATPASE ACTIVITY AND THEREBY REGULATES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
MEDLINE-89377832; PubMed-2776758;
Inoue A., Yanagisawa M., Takano-Ohmuro H., Masaki T.;
"Two isoforms of smooth muscle myosin regulatory light chain in
                                                                                                                                                                                                                                                                                                                             SUBUNIT: Myosin is an hexamer of 2 heavy chains and 4 light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.8%; Score 44; DB 1; Length 171; 47.6%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                         -!- MISCELLANEOUS: THIS CHAIN BINDS CALCIUM.
-!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACETYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY MLCK)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (BY MLCK) (BY SIMILARITY). EF-HAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47926518F95CCC78 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 EI
19780 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P13543; 1SCM.
InterPro; IPR002048; EF-hand.
Pfam; PF00036; efhand; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD000012; EF-hand; 2.
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18
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171 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
es 10; Conserv
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Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database.

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Q9jw24 neisseria m
Q86129 yersinia pe
Q82dio yersinia pe
Q55490 lactobacill
O96737 plasmodium
Q9rhb7 bradyrhizob
Q9rd88 streptomyce
Q9x878 delphinapte
Q9sx78 arabidopsis
                                                                                            Q9guaz riftia pach
Q28774 archaeoglob
Q8tr29 methanosarc
002134 caenorhabdi
Q95200 bacteriopha
Q95me8 homo sapien
Q94fwl abies grand
Q38710 abies grand
Q9haq7 homo sapien
Q81n05 drosophila
                                                                                                                                                                                                    Q9ijr3 human immun
Q9juf9 neisseria m
Q97y91 sulfolobus
Q96y98 sulfolobus
Q8g6t2 bifidobacte
Q9emu0 amsacta moo
                                                                                                                                                                                                                                                                   OBpuj3 methanosarc
OBsvw7 encephalito
OBefu3 shewanella
                                                                                                                                                                                                                                                                                                   Q8zws9 pyrobaculum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hisatomi H., Nagao K., Kanamaru T., Hirata H., Miyachi K., Hikiji H.;
"Exon 11 deleted variant of human reverse transcripatse.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB086950; BAC11015.1;
InterPro; IPR003545; Telomerase_RT.
PRINTS; PR01365; TELOMBRASERT.
SRQUENCE 795 AA, 88965 MW; 6BBACBA6D1A2EBCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MRR-2003 (TrEMBLrel. 23, Last annotation update)
ABG-deleted variant of telomerase reverse transcriptase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 130; DB 4;
Pred. No. 1.1e-11;
                                                                                                                                                                                                                                                                                                                                                                                      795 AA.
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                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
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                                                            Q9RDK8
Q9XS78
Q9SKX8
Q9GUA2
                                                                                                                 Q8TR29
Q02134
Q97200
Q94FW1
Q34FW1
Q9HAQ7
Q9HAQ7
Q91JR3
Q9JUF9
Q9TJP9
Q9TY91
Q9GGT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QBN6C3 PRELIMINARY; PRT; QBN6C3; 01-OCT-2002 (TrEMBLrel. 22, Created)
                               Q59490
O96737
Q9RHB7
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100.0%;
Best Local Similarity 100.0%;
Matches 27; Conservative 0
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116
116
110
110
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115
117
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117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=Stomach;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
 RESULT 1
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 OBN6C3
ID OE
AC OE
DT 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8ng38 homo sapien
Q8n6c3 homo sapien
Q9ng46 homo sapien
Q9jk99 rattus norv
Q9dx24 mesocricetu
Q9de32 xenopus lae
Q9eui0 salmonella
Q9jzc0 neisseria m
Q9jzc0 neisseria m
Q9fzx7 streptomyce
Q8fkv1 rhizobium e
Q8f5k1 leptospira
Q055k1 leptospira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9dc29 mus musculu
Q90rh2 human immun
Q9jxu5 neisseria m
                                                                   2003, 19:42:29; Search time 25.8113 Seconds (without alignments) 269.937 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                   1 ARTFREKRAERLTSRVKALFSVLNYE 27
                                                                                                                                                                                        830525 segs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Q9JK99
Q9DXZ4
Q9DE32
Q9EUIO
Q9JZCO
Q9JZCO
Q8FSK1
Q8F5K1
Q8F5K1
Q9F5K2
Q9FSCQ
                                                                                                                                                                Gapop 10.0 , Gapext 0.5
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sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*
sp_rodent:*
sp_virus:*
sp_virus:*
sp_vorlebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                  sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_bacteriap:*
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sp_bacteria:*
sp_fungi:*
                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                     November 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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1128
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554
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339.66
337.77
36.9
36.9
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51.5 51.5 51

Score

Result

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SEQUENCE FROM N.A.
MEDLINE=21240330; PubMed=11342218;
AGO W., Okamoto M., Lee Y.M., Baluda M.A., Park N.H.;
"Enhanced activity of cloned hamster TERT gene promoter in transformed
                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 575;
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RNA-directed DNA polymerase; Transferase.
SEQUENCE 1128 AA; 128394 MW; 1D4F81249012174E CRC64;
                                                                                                                                                                                wong S., Gao S., Xu X., Yu H.; "ITERT."; "Rat Lelomerase catalytic subunit, rTERT."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF247818; AAF62177.1; "InterPro; IPR00047; RVTse. InterPro; IRR003545; Telomerase_RT. Pfan; PF00078; rVt; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               575 AA; 65672 MW; F80C81BD7F6A91A3 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
10-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Telomerase reverse transcriptase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.2%; Score 73; DB 11;
53.8%; Pred. No. 0.0068;
tive 4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1191 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01365; TELOMERASERT.
RNA-directed DNA polymerase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            636 RAFDKGKQAQHFTQCLKTLFSVLNYE 661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Telomerase catalytic subunit.
Mesocricetus auratus (Golden hamster)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF149012; AAF17334.1; -.
InterPro; IPR000477; RVTse.
InterPro; IPR003545; Telomerase_RT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
   Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00078; rvt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mesocricetus.
NCBI_TaxID=10036;
                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9DE32
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Q9QXZ4
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0
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Stomach cancer;
Hisatomi H., Nagao K., Kanamaru T., Sumida H., Hirata H., Yamamoto M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
VCBI_TaxID=9606;
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                  "Both beta and gamma deletion isoform of human telomerase reverse transcriptase.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 130; DB 4; Length 807; Pred. No. 1.1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hisatomi H., Nagao K., Hirata H., Hikiji K., Kanamaru T., "Exon 11 deleted variant of the human telomerase reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AB085628; BAC11010.1; ...
InterPro; IPR003545; Telomerase_RT.
PRINTS; PR01365; TELOMESERT.
RNA-directed DNA polymerase.
SEQUENCE 1069 AA; 120047 MW; BEIE77A653BIC666 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB086379; BAC11014.1; -.
InterPro; IPR003545; TelOmerase_RT.
PRINTS; PR01365; TELOMERASERT.
SEQUENCE 807 AA, 90225 MW; 199664460CE6D763 CRC64;
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Beta and gamma deletion isoform of telomerase reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 130;
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Best Local Similarity 100.
Matches 27; Conservative
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                                                                                                                                                                Homo sapiens (Human)
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Gaps

Telomerase catalytic subunit (Fragment)

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Query Match

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Matches

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RESULT 3 **Q8NG46**

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Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Petterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C., "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                            STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E.; Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan B., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
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Neisseriaceae; Neisseria.
NCBI_TaxID=491;
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                                                                                                                                                                                                                                                                                                                         EMBL; AE006471; AAL23534.1; -.
InterPro; IPR001584; Rve.
Pfam; PF00665; rve; 1.
Plasmid; Complete Protecome.
SEQUENCE 554 AA; 63738 MW; AODB885C18031190 CRC64;
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98. AA; 11432 MW; E5DC7F0CF6115EA3 CRC64;
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Last sequence update)
Last annotation update)
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10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 51.5; |
Pred. No. 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        432 RTFRRGKAAER-ADRIHALAROLN 454
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MEDLINE=20175755; PubMed=10710307;
           Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2000 (TrEMBLrel. 15, Cr
01-0CT-2000 (TrEMBLrel. 15, Le
01-DEC-2001 (TrEMBLrel. 19, Le
Hypothetical protein NMB1120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.68;
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TIGR; NMB1120;
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Best Local Similarity 36.0%,
-hea 9; Conservative
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es 14; Conservative
                                                                                                                                                                                                                                                                                                         Nature 413:852-856(2001)
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                                                                             FROM N.A.
                                 NCBI_TaxID=602;
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SEQUENCE 98
                                                                             SEQUENCE
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Q9JZC0
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Haneda T., Okada N., Nakazawa N., Kawakami T., Danbara H.;
Haneda E., Okada N., Nakazawa N., Kawakami T., Danbara H.;
"Complete DNA Sequence and Comparative Analysis of the 50-Kilobase
Virulence Plasmid of Salmonella enterica Serovar Choleraesuis.";
Infect. Immun. 69:2612-2620(2001).
EMBL; AB040415; BAB20554.1;
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                 46.9%; Score 61; DB 13; Length 1191;
                                                                                                                                                                              "Telomerase reverse transcriptase of Xenopus laevis."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF212299; AAG43537.1; -
InterPro; IPR00477; RVTse.
InterPro; IPR003545; Telomerase_RT.
Pfam; PR00078; rvt; 2.
PRINTS; PR01365; TELOMERASERT.
RNA-directed DNA polymerase; Transferase.
SEQUENCE 1191 AA; 138016 MW; 9BD9D776869A57D6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
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Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Mismatches
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704 QEKKIHHFSSQIRNLFSVLNYE 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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NCBI_TaxID=119912;
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2002 (TrEMBLrel. 21,
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RLGA OR PSLT044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella enterica subsp.
                                                                                                                                    SEQUENCE FROM N.A.
Kuramoto M., Ishikawa F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 50.0
18s 11; Conservative
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Matches 14; Conservative
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Plasmid pSLT.
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                                                                         Xenopodinae; Xenopus.
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                                                                                         NCBI_TaxID=8355
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Q9EUIO;
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"Sequence, localization and characteristics of the replicator region of the symbiotic plasmid of Rhizobium etli."; Microbiology 143:2825-2831(1997).
                                                                                                                                                                                                          Girard M.L., Flores M., Brom S., Romero D., Palacios R., Davila G.; "Structural complexity of the symbiotic plasmid of Rhizobium leguminosarum bv. phaseoli."; J. Bacteriol. 173:2411-2419(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quintero V., Cevallos M.A., Davila G.,
"A site-specific recombinase and RecA are required to exert
incompatibility towards the symbiotic plasmid of Rhizobium etli.",
Submitted (JUN-2002) to the EMBL/GenBank/DDBU databases.
EMBL, U80928; AAMS5029.1;
                    Plasmid symbiotic plasmid p42d.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97419521; PubMed=9274036;
Ramirez-Romero M.A.; Bustos P., Girard L., Rodriguez O.,
Cevallos M.A., Davila G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Plasmid.
SEQUENCE 190 AA; 21230 MW; 448E0069C5DF232D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.7%; Score 49;
50.0%; Pred. No.
                                                                                                                                                                                         MEDLINE=91193195; PubMed=2013564;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leptospira interrogans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                            NCBI TaxID=29449;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CFN42;
                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CFN42;
                                                                                                                                                                     STRAIN=CFN42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Redenbach M., Kieser H.M., Denapaite D., Bichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of cordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandraam M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
-:- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <del>.</del>
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                                                                                                                                            SCO1193 OR SCG11A.24C.
Streptcomyces coellicolor.
Bacteria, Actinobacteria, Actinobacteriaes
Streptomycineae, Streptomycetaceae, Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=A3(2);
Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Transcription regulation; Complete proteome.
189 AA; 20687 MW; 2EC75D53C59259B8 CRC64;
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                      01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Putative tetR-family transcriptional regulator.
  189 AA.
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                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97000351; PubMed=8843436;
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EMBL; AL939108; CAB61605.1;
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DNA-binding; Transcriptio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Conservative
PRELIMINARY;
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                                                                                                                                                                                                                                              NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                    STRAIN=A3 (2);
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Matches
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Gaps

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DB 2; Length 190; 6; Indels

13;

4; Mismatches

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Gaps
                                                                                                            Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
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                                                                                                                                                             STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
Ren S.;
                                                                                                                                                                                                                                                              37.7%; Score 49; DB 16; Length 601; 39.1%; Pred. No. 42;
                                                                                                                                                                                                                                                                                           8; Indels
                                                                                                                                                                                             Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                       EMBL, AEO11345, AAN48879.1; ... Aminoacyl-tRNA synthetase; Ligase; Complete proteome. SEQUENCE 601 AA; 69124 MW; 59A5A4DFED3AD845 CRC64;
                           01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
  601 AA
                                                                                                                                                                                                                                                                                             6; Mismatches
                                                                  Aspartyl-tRNA synthetase (EC 6.1.1.12)
ASPS OR LA1680.
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Best Local Similarity 39.1%;
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RESULT 13

Last sequence update) Last annotation update)

Created) PRT;

(TrEMBLrel. 22, (TrEMBLrel. 22, I (TrEMBLrel. 23, I

QBKKV1; 01-OCT-2002 (TrEMBLrel 01-OCT-2002 (TrEMBLrel 01-MAR-2003 (TrEMBLrel Hypothetical protein. YP085.

GERAAGE

190 AA

PRELIMINARY;

Q8KKV1

RESULT 11 Q8KKV1

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52.9%;
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                                                                  Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 37.5
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                                                                                                                                                                                                                                                                                                                                               842 AA;
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Best Local Similarity
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VPU.
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Q90RH2
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KRAIN-CSTBL/63; TISSUE-Lung;

A Krawa J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Erkunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Rondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Rondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

A Pleischmann W., Gasaterland T., Gissi C., King B., Kochiwa H.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Liyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
                                                                                                                                                                                              MEDLINE=99381042; PubMed=9705847;

A Hirsch-Ernst K.I., Gaini-Rahimi S., Ernst B.P., Schmitz-Salue C.,
Hirsch-Ernst K.I., Gaini-Rahimi S., Ernst B.P., Schmitz-Salue C.,
Hirsch-Ernst K.I., Gaini-Rahimi S., Ernst B.P., Schmitz-Salue C.,
Bluchen Sipphys Res. Commun. 249:151-155(1998).

I Hochen. Biophys. Res. Commun. 249:151-155(1998).

I SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.

EMBL; AJ003004; CAA05793.1; -.

InterPro; IPR00149; ABC TM transpt.

InterPro; IPR00149; ABC TM transpt.

InterPro; IPR001439; ABC TM transpt.

R Pfam; PF00065; ABC TEANSPORTER.

R Pfam; PF000065; ABC TEANSPORTER.

R Pfam; PF000065; ABC TEANSPORTER.

R PMAN; SW00006; ABC transporter; 1.
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 23, Last annotation update)
1200005B17Rik protein (RIKEN cDNA 1200005B17 gene).
ABCBG OR 1200005B17RIK.
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinee; Mus.
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                                                              Last sequence update)
Last annotation update)
                   836 AA
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                                                Created)
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                 PRT;
                                                           01-AUG-1998 (TrEMBLrel. 07, 01-MAR-2003 (TrEMBLrel. 23,
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                 PRELIMINARY;
                                                                                                          Rattus norvegicus (Rat)
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                           ABC transporter.
                                              01-AUG-1998
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Gaps
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Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,

Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,

N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,

Hayami M., Ichimuza H., Parra J.H.,

"Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in

Republic of Congo-Brazzaville.";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF127546; AAK84902.1;

InterPro; IFR002094; Vpu.

Feam; PF00558; Vpu; 1.

SEQUENCE 81 AA; 9199 MW; A174A88997FE5119 CRC64;
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59;
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Pred. No. 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                           Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO04605; BAB24404.1;
EMBL; BC006634; AAH06634.1;
MGD; MGI:1921354; Abcb6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93770 MW; 5B8E1653011A4C0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.7%; Sco. 37.5%; Pred. No. 55, 37.5%; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 AA
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                                                                                                                                                                                                                                                                                              InterPro; IPR003593; AAA_ATPase.
InterPro; IPR001140; ABC_TM transpt.
InterPro; IPR001409; ABC_TM transpt.
Pfam; PF00664; ABC_membrane; 1.
Pfam; PF000005; ABC_tran; 1.
ProDom; PD000006; ABC_tran; 1.
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00211; ABC TRANSPORTER; 1.
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ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California
US-08-974-549A-613
US-08-912-951-325
US-08-912-951-324
US-08-912-951-314
US-08-912-951-314
US-08-912-951-314
US-08-912-951-314
US-08-912-951-314
US-08-912-951-310
US-08-912-951-30
US-08-912-951-30
US-08-912-951-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTATION NUMBER: 35,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nakamura, Toruna
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25.APR-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-851-843A-115;
Sequence 115, Application US/08851843A
Patent No. 6093809;
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 115:
   1189
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Sequence 235, App
Sequence 115, App
Sequence 115, App
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Sequence 217, App
Sequence 225, App
Sequence 2, Appli
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Sequence 225, App
Sequence 225, App
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Sequence 323, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                     November 12, 2003, 19:43:50 ; Search time 13.0314 Seconds (without alignments) 90.911 Million cell updates/sec
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Sequence 13, A
Sequence 60, A
Sequence 5, App
Sequence 217,
Sequence 217,
Sequence 217,
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Sequence 2
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-974-5549A-235
US-08-974-95-9115
US-09-430-323-115
US-08-974-95-91-13
US-08-974-95-91-13
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US-08-951-843A-217
US-08-974-549A-344
US-08-974-549A-344
US-08-974-549A-344
US-08-974-549A-344
US-08-974-549A-325
US-09-128-354-2
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US-08-974-549A-611
US-08-912-951-323
                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                              1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
                                                                                                                                                                                                                                                                                                                   328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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                                                                                                                         on:
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No.
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
COMPUTER: DatentIn PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FLING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRING APPLICATION: 536
PRING DATE: 06-MAY-1997
FLING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 146; DB 3;
Best Local Similarity 100.0%; Pred. No. 9e-16;
Matches 28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                         NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REPERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
                    FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple Panday
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKFLHWLMSVYVVELLRSFFYVTETTFØ 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States of America ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 115, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cech, Thomas R. APPLICANT: Lingner, Joachim APPLICANT: Nakamura, Toru APPLICANT: Chapman, Karen B. APPLICANT: Morin, Gregg B. APPLICANT: Harley, Calvin
                                                                                                                                                                                            TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 235
SEQUENCE CHARACTERISTICS:
LENGTH: 28 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
  01-OCT-1997
FILING DATE: 01-OCT-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W
FILING DATE: 01-OCT-1
                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-235
                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS:
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APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Keren B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrew, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend ...
STRFFT
                                                                                                                                                                               100.0%; Score 146; DB 3; Length 28; 100.0%; Pred. No. 9e-16;
                                                                                                                                                                                                                          0; Indels
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COUNTRY: USA

ZIP: 9411-3834

COMPUTER REDABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: Datentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION UNDER: US/08/974,549A

"ILING DATE: 19-NOV-1997

"TLING DATE: 19-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO PCT/US97/17618
                                                                                                                                                                                                                                                                                               1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
                                                                                                                                                                                                                                                                      1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
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FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAX-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
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APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/1'
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 235, Application US/08974549A Patent No. 6166178 GENERL INFORMATION: APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 28; Conservative
                         28 amino acids
  SEQUENCE CHARACTERISTICS
                                         TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
US-08-974-549A-235
                                                                                                                                   US-08-851-843A-115
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Gaps
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100.0%; Pred. No. 9e-16;
Mismatches 0; Indels
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CURRENT APPLICATION DATA:
PELLCATION NUMBER: US/08/851,843A
FILING DATE: 06-WAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
ITILE OF INVENTION: No. 6093809e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 115:
                                                                                                                                                                                                                                                                                                                                                                                            1 AKFLHWLMSVYVVELLRSFFYVTETTFO 28
                                                                                                                                                                                                                                                                                                                                                                   1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
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CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
APPLICATION NUMBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: United States of America ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 67, Application US/08851843A Patent No. 6093809
       (415) 576-0200
                                                                                                                  TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                               LENGTH: 28 amino acids
                         TELEFAX: (415) 576-03(
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36,429
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Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,4 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 01-OCT-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morin, Gregg B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 6
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 28, Conservative
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    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 146; DB 3;
; Pred. No. 9e-16;
0; Mismatches C
                                                          NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INPORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acids
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
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PAPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States of America ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 115, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
Lingner, Joachim
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 01-OCT-1996
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01-OCT-1996
              CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
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Gaps
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ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION DATA:
APPLICATION DATA:
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Peptide LOCATION: 1.129 OTHER INFORMATION: /note= "TRT motifs from human" US-08-974-549A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 67, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Chapmar, Yoru
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 146; DB 3;
Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, 8th Floor
          APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-0CT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-0CT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REPERRENCE/DOCKET NUMBER: 36,429
REPERRENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                         015389-002610US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
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STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
STREET: TWO
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APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: California
COUNTRY: USA
ZTATE: California
COUNTRY: USA
ZTATE: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-NEN-1997
FILING DATE: 25-APR-1997
FILING DATE: 25-APR-1997
FILING DATE: 18-NAV-1997
FILING DATE: 14-NG-1997
                                                                                                                                                                       /note= "TRT motifs from human"
                                                                                                                                                                                                                                                   Score 146; DB 3;
Pred. No. 4.9e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: Prancisco STATE: California
                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                       1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
                                                                                                                                                                                                                                                                                                                                                                                                    1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/08974549A Patent No. 6166178 GENERAL INFORMATION:
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%;
Matches 28; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                   ; NAME/KEY: Peptide
; LOCATION: 1..129
; OTHER INFORMATION:
US-08-851-843A-67
amino acid
                    STRANDEDNESS:
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APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calinam H.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
TITLE OF INVENTION: THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-4UG-1997
CLASSIFICATION 35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION 435
PRIOR APPLICATION 1435
PRIOR APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                          NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 146; DB 4;
Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSEE: Townsend and Townsend and Crew LLP ?: Two Embarcadero Center, 8th Floor San Francisco
                            APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
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                                                                                                                                                                                                                                     TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/08912951
Patent No. 6475789
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingmar, Joachim
APPLICANT: Lingmar, Joachim
APPLICANT: Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                      'OPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United Stat
ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
STREET: Tw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-430-323-67
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MEDIUM TYPES FLODEY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/430,323

FILING DATE: 29-Oct-1999

CLASSIFICATION: UNKNOWN>

PRIOR APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/851,843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "TRT motifs from human'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andrews, William H.
DF INVENTION: No. 6309867el Telomerase OF SEQUENCES: 225
                                                                          CLASSIFLALLOW: 3.50
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY ABORN INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
                       US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 67, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
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Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Morin, Gregg B.
Harley, Calvin
                                   18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1.129
; OTHER INFORMATION:
US-08-854-050-67
                          APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Peptide
                                           FILING DATE: 18
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-430-323-67
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GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Aramura, Toru
APPLICANT: Marian, Gregg B.
APPLICANT: Harley, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
ITILE OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATIVE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 5, Application US/08974549A ; Patent No. 6166178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
                                        JS-08-974-549A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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APPLICANT: Long, David M.
APPLICANT: Long, David M.
APPLICANT: Love, Ruschelle A.
TITLE OF INVENTION: Telomerase Reverse Transcriptase (TERT) Genes FILE REFERENCE: 47714-5009-US
CURRENT APPLICATION NUMBER: US/09/417,485D
CURRENT FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.1
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100.0%; Score 146; DB 4; Length 364;
Best Local Similarity 100.0%; Pred. No. 1.5e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 146; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 28; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION UNBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION 1435
PRIOR APPLICATION 1435
PRIOR APPLICATION 1435
PRIOR APPLICATION WHERE: US 08/724,643
PRIOR APPLICATION 1435
PRIOR APPLICATION 1435
PRIOR STRICK 100 NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 15.576
REGISTATION NUMBER: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKFLHWLMSVYVVELLRSFFYVTETTFQ 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
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OTHER INFORMATION: Partial TERT sequence
US-09-417-485D-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 40, Application US/09417485D Patent No. 6541202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEO ID NO 40
LENGTH: 364
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-09-417-485D-40
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100.0%; Score 146; DB 3; Length 1003; 100.0%; Pred. No. 4.7e-14;
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                                                                                                                                                                                                                                                                                     542 AKFLHWLMSVYVVELLRSFFYVTETTFQ 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 217, Application US/08851843A
Patent No. 6093809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFRENCE/DOCKET NUMBER: 015:
TELECOMMUNICATION INFORMATION:
TELEPAN: (415) 576-0200
INFORMATION FOR SEQ ID NO: 217:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Two Embarcade CITY: San Francisco STATE: California COUNTRY: United State
                               , MOLECULE TYPE: protein US-08-912-951-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
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Best Local Similarity
         linear
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US-08-851-843A-217
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         TOPOLOGY:
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APPLICANT: Coch, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND TITLE OF INVENTION: THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS: ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STREET: Chiffornia
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                                                                                                                            Gaps
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                                                      Query Match
Best Local Similarity 100.0%; Score 146; DB 3; Length 807;
Best Local Similarity 100.0%; Pred. No. 3.7e-14;
Matches 28; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CUUNTRY: United States of America
CUUNTRY: United States of America
ZIP: 94111

ZIP: 94111

MEDIUW TYBE: FIPOPDY disk
COMPUTER READABLE FORM:
OBERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION NUMBER: US 08/851,843
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/144,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: US 08/724,643
                                                                                                                                                                                                                     542 AKFLHWLMSVYVVELLRSFFYVTETTFO 569
                                                                                                                                                                                  1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08912951
Patent No. 6475789
GENERAL INFORMATION:
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TELEFAX: (415) 576-0300
INPERATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 807 amino acids TYPE: amino acid
US-08-974-549A-5
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Length 807;
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MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION
PRIOR APPLICATION
PRIOR APPLICATION
PRIOR APPLICATION OF THE TRANSPORT OF THE T
Query Match 100.0%; Score 146; DB 4; Best Local Similarity 100.0%; Pred. No. 3.7e-14; Matches 28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Townsend and Townsend and Crew LLP Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Nakamura, Toruna
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
CORRESPONDENCE ADDRESS:
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Gaps
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                                                                                                                                                                                                                                                     Length 1003;
                                                                                                                                                                                                                                                                                                           Indels
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SOFTWARE: Patentin Release #1.0; Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/861,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION: 536
CLASSIFICATION: 536
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INCORMATION:

APPLICANT: Cech, Thomas R.

APPLICANT: Clapman, Karen B.

APPLICANT: Chapman, Karen B.

APPLICANT: Chapman, Karen B.

APPLICANT: Chapman, Karen B.

APPLICANT: Harley, Calvin

APPLICANT: Harley, Calvin

APPLICANT: Harley, Calvin

APPLICANT: Andrews, William H.

ITITLE OF INVENTION: No. 6261836el Telomerase

NUMBER OF SEQUENTION: No. 6261836el Telomerase

NUMBER OF SEQUENTION

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COMPUTER REABABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: Delasse HI O' Varsion HI 30
                                                                                                                                                                                                                                                     Score 146; DB 3;
Pred. No. 4.7e-14;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION ST6-0200
TELECTAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 217:
                                                                                                                                                                                                                                                                                                                                                                                                                  413 AKFLHWLMSVYVVELLRSFFYVTETTFO 440
                                                                                                                                                                                                                                                                                                                                                              1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 217, Application US/08854050 Patent No. 6261836
                                                                                                                                                                                                                                                        Query Match 100.0%; Some Best Local Similarity 100.0%; P. Matches 28; Conservative 0;
                     INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1003 amino acids
(415) 576-0300
                                                                                                                                                                            , MOLECULE TYPE: peptide US-08-974-549A-336
                                                                                                 TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-854-050-217
TELEFAX:
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  Gaps
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  Indels
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APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
RIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
  Mismatches
                                                                                413 AKFLHWLMSVYVVELLRSFFYVTETTFQ 440
                                                   1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR PREDICATION DATA:
PRIOR DATE: 06-MAY-1997
PRIOR APPLICATION NUMBER: US 08/851,843
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
PRIOR APPLICATION NUMBER: US 08/911,312
PRIOR APPLICATION NUMBER: US 08/912,951
PRIOR APPLICATION NUMBER: US 08/912,951
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Orbanas Patentas
SOFTWARE: Patentas
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
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FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                               Sequence 336, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: CANAZIONE STREET 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIble
;
                                                                                                                                                                                                                                                                                                              Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
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Conservative
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CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC
OPERATING SYSTEM:
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US-08-974-549A-336
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APPLICANT:
Matches
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| SEQUENCE CHARACTERISTICS:
| LENGTH: 1003 amino acids | TYPE: amino acids | TYPE: amino acids | TYPE: amino acid | TYPE: amino
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Sequence:

Run on:

Searched:

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Result

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Sequence 225, App
Sequence 2, Appli
Sequence 225, App
Sequence 225, App
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Sequence 2, Appl
Sequence 31, A
Sequence 225, A
Sequence 27, Appl
Sequence 57, Appl
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Sequence 325, 1
Sequence 325, 1
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COMPUTER: TBM PC Compatible
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC COMPATIBLE
CONTUMER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFTCATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020164786Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLP
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COMPUTER READABLE FORM:
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US-10-282-960-81
US-10-294-778-12
US-10-294-778-12
US-10-044-692-5
US-09-843-676-217
US-09-843-676-217
US-09-438-486-217
US-10-053-758-217
US-10-054-295-217
US-09-990-080-2
US-09-991-611-217
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US-10-295-681-57
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US-10-105-963-2
US-10-044-692-2
US-10-044-539-2
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    ALIGNMENTS

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Patent No. US20020164786A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
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   Sequence 115, App
Sequence 67, Appl
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| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-843-676-115.
US-09-766-253-115
US-09-438-486-115
US-10-053-758-115
US-10-054-295-115
US-10-054-644-1-1-15
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US-09-766-253-67
US-09-438-486-67
US-10-053-758-67
US-10-054-611-67
US-10-054-611-67
US-10-044-692-13
US-10-044-539-13
US-10-282-960-3
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                                                                                                                                                                                                                                                                             644079 segs, 171749292 residues
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                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
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146
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Match Length
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225, App 2, Appli 57, Appl 225, App App1

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APPLICANT: Andrews, William H.
ITILE OF INVENTION: Wo. US20030009019Alel Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: FLOPMY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATEMIN PC-DOS/MS-DOS
SOFTWARE: PATEMIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
FLING DATE: 12-NOV-1999
CLASSIFICATION S36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FLING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 10-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
FILING DATE: 01-OCT-1996
                                                                                                                                           Query Match 100.0%; Score 146; DB 10; Best Local Similarity 100.0%; Pred. No. 4.9e-14; Matches 28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
ZUUTRY: United States of America
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCET DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                       TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 115:
                                                                                                                                                                                                                                               1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
                                                                                                                                                                                                                                                                                             1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 115, Application US/09438486
Publication No. US20030009019A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS:
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Linguer. Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                               US-09-766-253-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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APPLICANT:
APPLICANT:
APPLICANT:
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COMPUTER: 18M PC compatible

COMPUTER: 18M PC compatible

COMPATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253

FILING DATE: 19-Jan-2001

CLASSIFICATION NUMBER: 08/846,017

FILING DATE: 1997-04-25

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregs B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. US20020187471A1e1 Telomerase
NUMBER OF SEQUENCES: 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 146; DB 10; Best Local Similarity 100.0%; Pred. No. 4.9e-14; Matches 28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION:
                                         NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States of America ZIP: 94111
                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 115:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 115, Application US/09766253 Publication No. US20020187471A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (415) 576-0200
                                                                                                                                                                                            INFORMATION FOR SEQ ID NO. 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acids
STRANDEDNESS: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                         ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                  US-09-843-676-115
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                                                                                                                                                                                                                                                                                                                                                                                          Andrews, William H.
TITLE OF INVENTION: No. US20030044953A1el Telomerase
NUMBER OF SEOUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 146; DB 15;
100.0%; Pred. No. 4.9e-14;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 015389-002930US
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0
      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: «Unknown»
PPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/054,295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-10-054-295-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                       1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
                                                 1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
                                                                                                                                                          RESUL: 5
US-054-295-115
Sequence 115, Application US/10054295
Fublication No. US20030044953A1
GENERAL INFORMATION:
HOPPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                    Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin ReCURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          Harley, Calvin
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                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28; Conservative
      Conservative
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Matches 28; Conserv
      28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
      Matches
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                                                                                       Length 28;
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cech, Thomas R.

APPLICANT: Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: No. US20030032075A1el Telomerase
                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California
                                                                                         ; DB 11;
4.9e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 146; DB 15;
Pred. No. 4.9e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
APPLICATION NUMBER: US 08/846,017
FILING DATE: 05-MRY-1997
FILING DATE: 15-APR-1997
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
APPLICATION NUMBER: US 08/844,419
APPLICATION NUMBER: US 08/844,419
                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                     Query Match
100.0%; Score 146;
Best Local Similarity 100.0%; Pred. No. 4
Matches 28; Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-10-053-758-115
                                                                                                                                                                                                1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
                                                                                                                                                                                                                                                                                                                         Sequence 115, Application US/10053758
Publication No. US20030032075A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
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100.0%;
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-438-486-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andrews, William H.
TITLE OF INVENTION: No. US20020187471A1el Telomerase
                     Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: US20020164786Alel Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                          Townsend and Crew LLP
                                                                                                                                             STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 146; DB 10;
ilarity 100.0%; Pred. No. 2.3e-13;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                    STATE: California COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
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Publication No. US20020187471A1
GENERAL INFORMATION:
Lingher, Joachim
Lingher, Joachim
NARAMUTA, Toru
Chapman, Karen B.
                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: <Unknown>
  Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morin, Gregg B.
Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                     CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1..129
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                              ZIP: 94111
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                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                          Andrews, William H.
TITLE OF INVENTION: No. US20030059787A1el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; DB 15;
4.9e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-10-054-611-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 146; 100.0%; Pred. No. 4
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                 Sequence 115, Application US/10054611 Publication No. US20030059787A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 67, Application US/09843676
Patent No. US20020164786A1
GENERAL INFORMATION:
                                                                            APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 115:
                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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Best Local Similarity 100.
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELEFAX:
US-10-054-611-115
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Andrews, William H.
TITLE OF INVENTION: No. US20030032075Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                         CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
CLASSIFICATION DATA:
APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
CLASSIFICATION S36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION S36
PRIOR APPLICATION NUMBER: US 08/846,017
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
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LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 146; DB 11; Best Local Similarity 100.0%; Pred. No. 2.3e-13; Matches 28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 67, Application US/10053758;
Publication No. US20030032075A1;
GENERAL INFORMATION:
APPLICANT: Cach, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 129 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-10-053-758-67
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                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OMPERATING SYSTEM: PC-DOS/MS-DOS
OMPERATING SYSTEM: PC-DOS/MS-DOS
OMPWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION NUMBER: 08/846,017
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 19-97-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 19-07T-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELEPONE: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1.129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cech, Thomas R.
APPLICANT: Cech, Thomas R.
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Foru
APPLICANT: Chapman, Karen B.
APPLICANT: Andrews, William H.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US20030009019A1e1 Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
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                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 146; DB 10;
; Pred. No. 2.3e-13;
0; Mismatches 0;
                                                                                                                                           STATE: California
COUNTRY: United States of America
ZIP: 94111
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; Sequence 67, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 28; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 576-0
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
NUMBER OF SEQUENCES: 171
                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94111-3834
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) LOCATION: 1..129
); SEQUENCE DESCRIPTION: SEQ ID NO: 67:
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Andrews, William H.
TITLE OF INVENTION: No. US20030059787A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 146; DB 15; Best Local Similarity 100.0%; Pred. No. 2.3e-13; Matches 28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: «UnKnown»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 01-OCT-1996
                                                                                                               CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
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COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 129 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
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SEQUENCE CHARACTERISTICS
COMPUTER READABLE FORM:
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MOLECULE TYPE: peptide
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OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030044953A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFRENCE/DOCKET NUMBER: 015389-002930US
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 146; DB 15; Best Local Similarity 100.0%; Pred. No. 2.3e-13; Matches 28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/654,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
APPLICATION NUMBER: US 08/724,643
APPLICATION NUMBER: US 08/724,643
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIPICATION: 536
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STATE: California
COUNTRY: United States of America
ZIP: 94111
  COUNTRY: United States of America
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Publication No. US20030044953A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 67:
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                          ZIP: 94111
COMPUTER READABLE FORM:
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MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
US-10-054-295-67
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Length 129;

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Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                 NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 146; DB 15;
100.0%; Pred. No. 2.3e-13;
iive 0; Mismatches 0;
                                                                                                              APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAX-1997 FILING DATE: 06-MAX-1997 APPLICATION NUMBER: US 08/851,843 APPLICATION NUMBER: US 08/846,017 FILING DATE: 18-APR-1997 FILING DATE: 18-APR-1997
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                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: California
COUNTRY: United States of America
ZIP: 94111
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                                                                      APPLICATION NUMBER: 08/912,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/10044539 Publication No. US20030100093A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                              FILING DATE: <Unknown>
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
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OTHER INFORMATION:
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                                                 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ropology: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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Harley, Calvin
Andrews, William H.
TILE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1.129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 146; DB 15; Best Local Similarity 100.0%; Pred. No. 2.3e-13; Matches 28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                         NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THERAPEUTIC METHODS
                                                                                                                                                                            APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-ARR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-ARR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
                     SNT APPLICATION DATA:
PAPPLICATION NUMBER: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIPICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: United States of America
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APPLICATION NUMBER: US/10/044,692
                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/10044692;
Publication No. US20030096344A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 67: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
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Matches
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Search completed: November 12, 2003, 19:55:47 Job time: 22.3648 secs
                               3 AKFLHWLMSVYVVELLRSFFYVTETTFQ 30
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APPLICANT: Zhaoyang, You
APPLICANT: Schroers, Roland
TITLE OF INVENTION: Human Telomerase Reverse Transcriptase as a Class-II Restricted
TITLE OF INVENTION: Associated Antigen
FILE REFERENCE: P02193US1
CURRENT APPLICATION NUMBER: US/10/282,960
CURRENT FILING DATE: 2002-10-29
PRIOR PLING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-29
SOFTWARE: PARENT DATE: 2001-10-39
SOFTWARE: PARENT DATE: 2001-10-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 146; DB 15; Length 129; larity 100.0%; Pred. No. 2.3e-13; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 146; DB 12; Best Local Similarity 100.0%; Pred. No. 5.1e-13; Matches 28; Conservative 0; Mismatches 0;
                                                                                            APPLICATION NUMBER: 08/912,951
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/46,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US/10/044,539
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                          FILING DATE: 11-Jan-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acids
STRANDEDNESS: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/10282960
Publication No. US20030143228A1
GENERAL INFORMATION:
APPLICANT: Chen, Si-Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 28; Conserva
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; ORGANISM: Human
US-10-282-960-3
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Human telomerase r N-terminal truncat

CRT-1 protei

Sequence:

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Searched:

Database

Result No.

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Truncated telomera
Truncated telomera
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N-terminal truncat
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Human telomeraep
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Altered C-terminus
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Telomerase protein
Telomerase (ver. 2
Human telomerase c
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Heart muscle cell
Human telomerase r
Human telomerase r
Glutathione-S-tran
Human telomerase pr
Glutathione-S-tran
Telomerase pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                               AAW46957
AAY43621
AAY28881
AAY32090
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AAW90251
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AAU72735
ABP56676
              AAW46997
AAY00637
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AAY26580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0724643.
97US-0844419.
97US-0851843.
97US-0851843.
97US-0911312.
97US-0912951.
 97GB-0020890
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GERO-) GERON CORP
 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996;
18-APR-1997;
25-APR-1997;
06-MAY-1997;
09-MAY-1997;
14-AUG-1997;
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 Synthetic.
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 TO SEE THE SEE
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hTBRT fragment wit
Human telomerase r
Human telomerase r
Human CRT-1 protei
Human CRT-1 protei
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A catalytic telome
                                                                                                     November 12, 2003, 19:41:04 ; Search time 37.3585 Seconds (without alignments) 127.462 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                            A Geneseq 19Jun03:*

| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseqg-embl/AA1981.DAT:*
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                                                                                                                                                                                                                                                                                                              1107863
            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                 US-08-854-050-116
152
1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                            1107863 seqs, 158726573 residues
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Match 100%
first 45 summaries
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AAW97385
ABG71627
AAW46998
AAY43128
AAY43128
AAY25461
AAY25462
AAW56109
                                                                        OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
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1152
1145
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hEST2, a human tel Human telomerase r Human telomerase p

Gaps

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Length 131; Indels

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New catalytic protein of telomerase of a higher animal and a gene
                                                               Example 8; Fig 54; 387pp; English
                                                                                                                                                                                                                                                                               AAW97385 standard; Protein; 131
                                                                                                                                                                                                                                                                                                                                                                                                 (MITU ) MITSUBISHI CHEM CORP
(UYTE-) UNIV TECHNOLOGY CORP
                                                                                                                                                                                                                                                                                                                                                                                     97JP-0207708
                                                                                                                                                                                                                                                                                                     14-MAY-1999 (first entry)
                                                                                                                                                                                                                          30; Conservative
           , Cech TR,
Nakamura T,
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-208111/18.
                            WPI; 1998-171633/16.
                                                                                                                                                                                                              Ouery Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                    30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAX15924
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            Andrews WH,
                 Morin GB,
                                                                                                                                                                                                                                                                                          AAW97385;
                                                                                                                                                                                                    Sequence
                                                                                                                                                                                         methods
                                                                                                                                                                                                                                                                    RESULT 2
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The present invention relates to a polypeptide comprising a 20 amino acid sequence derived from human telomerase catalytic subunit (or human telomerase reverse transcriptase, hTRERT) amino acid residues 537-556, or fragments thereof comprising at least 10 amino acids and at least two human leukocyte antigen (HLA) class I or class II epitopes. The invention also describes a polypeptide having the above 20 amino acids peptide sequence as additional C and/or N-terminal sequences on a fragment of hTERT which is not more than 100 amino acids of hTERT. The polypeptides of the invention are useful in a pharmaceutical composition or in a vaccine for preventing or treating cancer in populations of individuals having varying HLA profiles. The polypeptides are also useful in a diagnostic kit for diagnosing cancers such as breast, pancreatic, colorectal, lung, ovarian or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; telomerase catalytic subunit; hTERT; human leukocyte antigen; human telomerase reverse transcriptase; HLA epitope; cancer; HLA profile; breast cancer; paracreatic cancer; cancer; cancer; lung cancer; novarian cancer; cervical cancer; malignant melanoma; leukaemia; lymphoma; bilary tract carcinoma; anti-cancer; mutant; cytostatic; HLA class I epitope; HLA class II epitope; mutein.
coding it - useful for diagnosis of diseases caused by the change in activity of a telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hTERT fragment with HLA containing polypeptide at its N-terminus.
                                                                                                                                                    The specification describes a human catalytic telomerase protein. The products are useful in drug compositions for the diagnosis of diseases caused by the change in activity of telomerase. The present sequence appears in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptide with an additional C-terminal and/or N-terminal sequence, useful for preparing anti-cancer vaccines
                                                                                                                                                                                                                                                                                                        100.0%; Score 152; DB 2u;
                                                                                                                                                                                                                                                                                                                                                       1 Similarity 100.0%; Pred. No. 1.2
30; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG71627 standard; protein; 100 AA
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                                                                                                        Example 1; Page 14; 18pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                 131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEMV-) GEMVAX AS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JAN-2003
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                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                  The present sequence represents an antigenic peptide from human telomerase reverse transcriptase (hTRT) from the present invention. The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein preparation of hTRT with a telomerase by contacting a protein preparation of hTRT with a telomerase by contacting a protein preparation of the hTRT with or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of hTRT in the sample, and (B) increasing the product with presence of hTRT in the sample, and (B) increasing the use of an agent that causes an increasing hTRT can be used in the manufacture of medicaments for inhibiting the ageing. A protein preparation of hTRT and the polynucleotide encoding hTRT can be used in the manufacture of medicaments for inhibiting the used to treat conditions that are associated with high telomerase contrainty. A protein preparation of hTRT can also be used in the new
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                                                                                                                                                                                                        Pure and recombinant human Telomerase Reverse Transcriptase and variants - are useful in the diagnosis, prognosis and treatment cell proliferation conditions especially cancer and ageing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 30;
                                                                                   Lingner J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 152; DB 19;
100.0%; Pred: No. 2.4e-16;
ive 0; Mismatches 0;
                                                                                   Harley C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
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                                                                                Chapman KB,
Harley CB;
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sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of HTRT in the sample; and (D) increasing the product with presence of HTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing HTRT expersion; and (E) the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polynucleotide encoding HTRT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions that are associated with high telomerase activity. A protein preparation of HTRT can also be used in the new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HTERT). The invention relates to a monoclonal antibody recognising the hTERT. The antibody can be used for the investigation, diagnosis and treatment of telomerase-related diseases, especially diseases in which telomerase expression is up-regulated e.g. cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New monoclonal antibody recognizing human telomerase catalytic subunit (hTERT) useful for treating and diagnosing cancer -
                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human telomerase reverse transcriptase; hTERT; antibody; diagnosis;
telomerase-related disease; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the human telomerase reverse transcriptase
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                                                                                                                                                                                                                                         ch 95.4%; Score 145; DB 19; Length 259; Similarity 93.3%; Pred. No. 3.2e-14; 28; Conservative 2; Mismatches 0; Indels (
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Pred. No. 3.5e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human telomerase reverse transcriptase
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                                                                                                                                                                                                                                                                                                                                                                                                              AAY43128 standard; Protein; 283
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hes 28; Conservative
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                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                             259 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Human telomerase reverse transcriptase protein from cDNA clone 712562.
tract carcinoma. The polypeptides or encoding polynucleotide sequences are useful for performing identity, sequence homology and/or hybridisation studies, for predicting structure and/or function (e.g. anti-cancer activity), or for screening methods in drug development or drug screening procedures. The present sequence represents a hTERT fragment with the 20 amino acid HIA epitope
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of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis;
prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
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                                                                                                                                                                            Length 100;
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                                                                                                                                                                          Score 145; DB 23;
Pred. No. 1.1e-14;
2; Mismatches 0
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Harley CB;
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                                                                                                                                                                                                                                                                                                                                           AAW46998 standard; Protein; 259
                                                                                                                                                                         Match 95.4%;
Local Similarity 93.3%;
Les 28; Conservative 2
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96US-0724643.
97US-0844419.
97US-0851843.
97US-0854050.
97US-091312.
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Nakamura T,
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N-PSDB; AAV22379.
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14-AUG-1997;
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18-APR-1997;
25-APR-1997;
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AAY25461 standard; Protein; 437 AA

AAY25461;

(first entry)

Human CRT-1 protein

Location/Qualifiers

Homo sapiens

1..437 /label= CRT-1

Protein

99WO-JP00039 98JP-0139177 98JP-0013232.

08-JAN-1999;

WO9935261-A1

(CHUS) CHUGAI SEIYAKU KK.

06-MAY-1998; 08-JAN-1998; 30-JAN-1998;

Tsuchiya M, Yoshida K;

WPI; 1999-430393/36.

N-PSDB; AAX88243.

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proteins containing a reverse transcriptase motif, which act as telomerase inhibitors. The gene, its encoded protein and derived antibodies can be used to provide base sequence information, detect telomerase activity and cancer cells, and to screen telomerase inhibitors. The detection method is simple and effective.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel human CRT-1 genes and their encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel gene, useful in detection of telomerase activity and cancer cells as well as screening telomerase inhibitors for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, telomerase reverse transcriptase, hTRT, TRT, diagnosis, prognosis, cell proliferation, cancer, ageing, ribonucleoprotein.
CRT-1; reverse transcriptase; telomerase; inhibitor; detection;
                                                                                                                                   /note= "Partial sequence, no stop codon given"
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                 telomerase activity; cancer cell; screening; human
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Best Local Similarity 93.3%; Pred. No. 5.7e-14;
Matches 28; Conservative 2; Mismatches 0;
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/label= encoded by ARG
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                                                                                    Location/Qualifiers
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/label= CRT-1
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98JP-0013232.
98JP-0033584.
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                                                                                                    Protein
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ID AAW5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel human CRT-1 genes and their encoded proteins containing a reverse transcriptase motif, which act as telomerase inhibitors. The gene, its encoded protein and derived antibodies can be used to provide base sequence information, detect telomerase activity and cancer cells, and to screen telomerase inhibitors. The detection method is simple and effective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel gene, useful in detection of telomerase activity and cancer cells as well as screening telomerase inhibitors for treatment of
                                                                                                                                                                                                      CRT-1; reverse transcriptase; telomerase; inhibitor; detection; telomerase activity; cancer cell; screening; human.
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Pred. No. 5.7e-14;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 LFFYRKSVWSKLQSIGIRQHLKRVQLRELS 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
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Claim 2; Page 31-32; 44pp; Japanese.

AAY25462 standard; Protein; 438 AA.

AAY25462

(first entry)

22-SEP-1999

Human CRT-1 protein #2.

95.4%;

437 AA;

Sequence Query Match 28; Conservative

Best Local Similarity

Matches

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New catalytic protein of telomerase of a higher animal and a gene coding it - useful for diagnosis of diseases caused by the change in activity of a telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel gene, useful in detection of telomerase activity and cancer
                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a catalytic telomerase protein. The products are useful in drug compositions for the diagnosis of diseases caused by the change in activity of telomerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        telomerase activity; cancer cell; screening; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.4%; Score 145; DB 20; 93.3%; Pred. No. 7.9e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 LFFYRKSVWSKLQSIGIRQHLKRVQLRELS
                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 11-14; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY25463 standard; Protein; 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..622
/label= CRT-1
                                                                                                                                                                      (MITU ) MITSUBISHI CHEM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98JP-0139177.
98JP-0013232.
98JP-0033584.
                                                                                            97JP-0207708
                                                                                                                                 97JP-0207708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 93.3°
....hes 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yoshida K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human CRT-1 protein #3.
                                                                                                                                                                                                         WPI; 1999-208111/18.
N-PSDB; AAX15923.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-430393/36.
N-PSDB; AAX88251.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       591 AA;
                                                                                              01-AUG-1997;
                                                                                                                                 01-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9935261-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JAN-1998;
30-JAN-1998;
                                                          23-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY25463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
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     8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a human telomerase reverse transcriptase (hTRT) clone protein from the present invention. The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polynucleotide, on administration of the compound, (B) preparation of Frecombinant telomerase by contacting a protein preparation of recombinant telomerase BNA component; (C) detection of the hTRT RNA or protein in sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of hTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTRT expression; and (E) the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polynucleotide encoding hTRT can be used in the manufacture of medicaments for inhibiting the teffect of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions that are associated with high telomerase conditions that are associated with high telomerase are not an expression of hTRT can also be used in the mean associated with high telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                             Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 564;
                                                                                                                                                                                                                                                                                                    Harley C, Lingner J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.4%; Score 145; DB 19;
ilarity 93.3%; Pred. No. 7.5e-14;
Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LFFYRKSVWSKLQSIGIRQHLKRVQLRELS 54
                                                                                                                                                                                                                                                                                                  Chapman KB,
Harley CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 68; 387pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW97384 standard; Protein; 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A catalytic telomerase protein.
                                                                                                                                                                                                                                          GERON CORP.
UNIV TECHNOLOGY CORP.
                                                                                       960S-0724643.
970S-0844419.
970S-0846017.
970S-0851843.
970S-0911312.
970S-0911312.
                                    97GB-0020890
                                                                                                                                                                                                                                                                                                , Cech TR,
Nakamura T,
                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-171633/16.
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Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          564 AA;
                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAV22426
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                                    01-OCT-1997;
                                                                                                                                                                                    14-AUG-1997;
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                                                                                           01-OCT-1996
08-APR-1998
                                                                                                                                                 06-MAY-1997
                                                                         14-AUG-1997
                                                                                                                             25-APR-1997
                                                                                                                                                                09-MAY-1997
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                                                                                                                                                                                                                                                                                                                     Morin GB,
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                                                                                                                                                                                                                                                             (UYTE-)
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preparation of recombinant telomerase by contacting a protein preparation of hTRT with a telomerase RNA component; (C) detection of preparation of hTRT with a telomerase RNA component; (C) detection of the hTRT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplification product with presence of hTRT in the sample; and (D) increasing the prodiferation of a vertebrate cell by increasing hTRT or presence of the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polymucleotide encoding hTRT and be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions that are associated with high telomerase controls.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia; neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma; smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour; stem cell differentiation; organ regeneration; organ differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is a truncated human telomerase of the invention. Primers that amplify the telomerase coding sequence can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated vertebrate telomerase genes - used to develop products for treating cancers or for organ regeneration, nerve cell or brain cell growth following injury or bone marrow transplantation
protein or polynucleotide, on administration of the compound; (B)
                                                                                                                                                                                                                                                                                                                                                                 / Match 95.4%; Score 145; DB 19; Local Similarity 93.3%; Pred. No. 1.1e-13; Les 28; Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-terminal truncated telomerase protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Fig 11d-e; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY00637 standard; Protein; 807 AA
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97US-0053018.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-106060/09.
                                                                                                                                                                                                                                                                                                                               807 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAX18265.
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                             methods
                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
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ID AAY(
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                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               its
                                                                                                                  proteins containing a reverse transcriptase motif, which act as telomerase inhibitors. The gene, its encoded protein and derived antibodies can be used to provide base sequence information, detect telomerase activity and cancer cells, and to screen telomerase
                                                                                                This invention describes novel human CRT-1 genes and their encoded
    벙
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pure and recombinant human Telomerase Reverse Transcriptase and variants - are useful in the diagnosis, prognosis and treatment cell proliferation conditions especially cancer and ageing
                                                                                                                                                                                                                                                                                                                 .;
0
    screening telomerase inhibitors for treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis;
                                                                                                                                                                                                                                                                       Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lingner J;
                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                              inhibitors. The detection method is simple and effective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human telomerase reverse transcriptase Delta182 variant.
                                                                                                                                                                                                                                                                         Score 145; DB 20;
Pred. No. 8.4e-14;
2; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                   1 LPFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
                                                                                                                                                                                                                                                                                                                                                                                           92
                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 37-39; 44pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW46997 standard; Protein; 807
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                                                                                                                                                                                                                                                                           95.4%;
93.3%;
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97US-0846017
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97US-0854050
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97US-0912951
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                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 93.33
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-AUG-1998 (first entry)
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Morin GB, Nakamura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1998-171633/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORP
                                                                                                                                                                                                                                     622 AA;
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      38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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18-APR-1997
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Synthetic

(UYTE-)

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used in a method for diagnosing cancer in a patient. The telomerase can be used for detection, diagnosis and drug screening. Inhibitors of telomerase activity can be used to treat cancers such as melanomas, other skin cancers, neuroblastomas, breast carcinomas, colon carcinomas, lackaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin growths. Enhancers of telomerase may be used to stimulate stem cells could be administered in the bone marrow transplant context). As well, many tissues have stem cells. Proliferation of these cells may be useful in wound healing, hair growth, treatment of disease such as Wilm's tumout, organ regeneration or differentiation after injury or diseases, nerve cell or brain cell growth following injury.
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                                                                                                                                                                                           95.4%; Score 145; DB 20; Length 807; 93.3%; Pred. No. 1.1e-13;
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                                                                                                                                                                                                                                                            573 LFFYRKSVWSKLQSIGIRQHLKRVQLRELS 602
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Matches 28; Conservative
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leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin growths. Enhancers of telomerase may be used to stimulate stem cell proliferation and differentiation (expansion of haematopoietic stem cells could be administered in the bone marrow transplant context). As well, many tissues have stem cells. Proliferation of these cells may be useful in wound healing, hair growth, treatment of disease such as Wilm's tumour, organ regeneration or differentiation after injury or diseases, nerve cell or brain cell growth following injury.
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cell proliferation and differentiation (expansion of haematopoietic stem cells could be administered in the bone marrow transplant context). As well, many tissues have stem cells. Proliferation of these cells may be useful in wound healing, hair growth, treatment of disease such as Wilm's tumour, organ regeneration or differentiation after injury or diseases, nerve cell or brain cell growth following injury.
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Truncated telomerase (ver. 2) protein sequence lacking motif A. 1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30 A. AAY00651 standard; Protein; 936 (first entry) 26-JUL-1999 AAY00651; RESULT 15 AAY00651 셤

Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia; neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma; smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour; stem cell differentiation; organ regeneration; organ differentiation.

97US-0058287. 98WO-US13835 01-JUL-1998; Homo sapiens WO9901560-A1 09-SEP-1997; 14-JAN-1999 Synthetic.

(CAMB-) CAMBIA BIOSYSTEMS LLC 97US-0051410. 97US-0053018. 97US-0053329. 97US-0054642. 21-JUL-1997; 21-JUL-1997; 04-AUG-1997;

01-JUL-1997;

Bowtell D, Kilian A;

WPI; 1999-106060/09. N-PSDB; AAX18279.

New isolated vertebrate telomerase genes - used to develop products for treating cancers or for organ regeneration, nerve cell or brain cell growth following injury or bone marrow transplantation Claim 4; Fig 11ak-al; 134pp; English.

This sequence is a truncated human telomerase of the invention. Primers that amplify the telomerase coding sequence can be used in a method for diagnosing cancer in a patient. The telomerase can be used for detection, diagnosis and drug screening. Inhibitors of telomerase activity can be used to treat cancers such as melanomas, other skin cancers, neuroblastomas, breast carcinomas, colon carcinomas, leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin growths. Enhancers of telomerase may be used to stimulate stem cell proliferation and differentiation (expansion of haematopoietic stem cells could be administered in the bone marrow transplant context). As well, many tissues have stem cells. Proliferation of these cells may be useful in wound healing, hair growth, treatment of disease such as

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             diseases, nerve cell or brain cell growth following injury. Note: The N-terminus of this sequence can be replaced by the sequences
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Wilm's tumour, organ regeneration or differentiation after injury or
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                                                                                                          95.4%; Score 145; DB 20; 93.3%; Pred. No. 1.3e-13; live 2; Mismatches 0;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/846,017
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
APPLICATION:
APPLICATIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cachim
APPLICANT: Cachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Greege B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
US-09-052-919-2
US-08-912-951-2
US-08-917-549A-611
US-08-917-551-323
US-08-912-951-325
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US-08-912-951-314
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REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INPORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 116:
                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
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; Sequence 116, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
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Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
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NAME: Apple, Randolph T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Apple, Randolph
REGISTRATION NUMBER: 36
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Sequence 217,
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Sequence 5, P
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              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-974-59A-236
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US-08-851-843A-67
US-08-974-549A-13
US-08-974-549A-13
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US-09-675-321-2
                                                                                                                                                                                                                                                                                                                    328717 segs, 42310858 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
Match Length
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                                                                                                                                                                                                                                                                Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                                      Run on:
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No.
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SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/854,050

FILING DATE: 09-MAY-1997

CLASSIFICATION 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

CLASSIFICATION 1536

PRIOR APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 152; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 116, Application US/08854050
Fatent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Chapmar, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Andrews, William H.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco CTATE: California COUNTRY: United States of America
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/ACENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEFORMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LFFYRKSVWSKLOSIGIROHLKRVOLRDVS 30
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-236
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-854-050-116
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; Sequence 236, Application US/08974549A
; Patent No. 616617B
; APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Makamura, Toru
APPLICANT: Mariey, Calvin B.
APPLICANT: Mariey, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTON: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
                                                                                                                                                                                                                                             100.0%; Score 152; DB 3; Length 30; 100.0%; Pred. No. 1.7e-16;
                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 1334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
RIUNG DATE: 25-APR-1997
PRIOR APPLICATION NUMBER: US 08/865,017
FILING DATA: 18-APR-1997
PRIOR APPLICATION NUMBER: US 08/851,843
APPLICATION NUMBER: US 08/851,843
APPLICATION NUMBER: US 08/851,937
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,050
FILING DATE: 14-ANG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-ANG-1997
RIUNG DATE: 14-ANG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-ANG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                     0; Mismatches
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APPLICATION NUMBER: WO PCT/US97/17618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-1997
                                      LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLLGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 30; Conservative
                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 14-AUG-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 14-AUG-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
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US-08-974-549A-236
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FILLING DATE: 05-MAY-1997
                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 152; DB 4; Best Local Similarity 100.0%; Pred. No. 1.7e-16; Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    015389-002930US
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                                                                                                                                                                                                                                                                                                                                                                           1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 116:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: APPLICATION NUMBER: 36,429
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: APPLICATION NUMBER: 36,429
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: 36,429
FILECOMMUNICATION INFORMATION:
TELEFHONE: (415) 576-0300
TELEFAX: 1000 67:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: California
COUNTRY: United States of America
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 67, Application US/08851843A; Patent No. 6093809
       TELEPHONE: (415) 576-0200
                                                                                                                   TYPE: amino acid
STRANDEDNESS: <Unknown>
                               TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coch, Thomas R. Lingner, Joachim Nakamura, Toru Chapman, Karen B. Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                    US-09-430-323-116
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APPLICANT:
APPLICANT:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: -UNknown>
PRIOR APPLICATION: -UNknown>
PRIOR APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 126-APR-1997
APPLICATION NUMBER: US 08/44,419
FILING DATE: 126-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 10-APR-1997
APPLICATION NUMBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 152; DB 3;
100.0%; Pred. No. 1.7e-16;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Andrews, William H.
INVENTION: No. 6309867el Telomerase
? SEQUENCES: 225
                                                         NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFENCE/COKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 116: SEQUENCE CHARACTERISTICS:
LENGTH: 30 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 116, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Randolph T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harley, Calvin
01-OCT-1996
N: 536
                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS:
                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-430-323-116
                                                                                                                                                                                                                                                                                                                                                              US-08-854-050-116
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Query Match 95.4%; Score 145; DB 3; Length 129; Best Local Similarity 93.3%; Pred. No. 1.1e-14; Matches 28; Conservative 2; Mismatches 0; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 25-APR-1997
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Peptide

| LOCATION: 1..129

| CTHER INFORMATION: /note= "TRT motifs from human"

US-08-974-549A-13
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                   PRILING DATE: 01-0CT-1997
PRIOR PAPLICATION NUMBER: W0 PCT/US97/17618
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: W0 PCT/US97/17885
FILING DATE: 01-0CT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
RECISTRATION NUMBER: 36,429
RECISTRATION NUMBER: 36,429
RECISTRATION NUMBER: 36,429
RECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TTYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chapman, Karen B.
APPLICANT: Worlin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 67, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Toru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 25-APR CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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US-08-854-050-67
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APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
ITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-000/1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,643
FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 13-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 35-APR-1997
APPLICATION NUMBER: US 08/845,843
                                                                                                                                                                         /note= "TRT motifs from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco CITY: California COUNTRY: USA
                                                                                                                                                                                                                                           Query Match
95.4%; Score 145; DB 3;
Best Local Similarity 93.3%; Pred. No. 1.1e-14;
Matches 28; Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                           1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
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APPLICATION NUMBER: US 08/915,503
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APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111-3834
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
MCDMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/08974549A Patent No. 6166178 GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                            MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                   LOCATION: 1.129
; OTHER INFORMATION:
US-08-851-843A-67
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                             NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-974-549A-13
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Gaps

; 0 us-08-854-050-116.rai

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Sequence 13, Application US/08912951
Patent No. 6475789
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Inigner, Joachim
APPLICANT: Nakamuza, Toru
APPLICANT: Marmuza, Toru
APPLICANT: Marmuza, Toru
APPLICANT: Mariey, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Harley Harley
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95.4%; Score 145; DB 4; Length 129;
Best Local Similarity 93.3%; Pred: No. 1.1e-14;
Matches 28; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1.129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIAL.

STAT:
STATE
STATE
STATE
STATE
COUNTRY: United State.
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PLILNG DATE: 14-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION UNMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION 0435
PRIOR APPLICATION 0435
PRIOR APPLICATION 1435
PRIOR APPLICATION DATE: US 08/851,843
FILING DATE: 06-MAY-1997
                                                 APPLICATION NUMBER: US 08/44,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSEE: Townsend and Townsend and Crew LLP
I: Two Embarcadero Center, 8th Floor
San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend &
STREET: Two Embarcade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-430-323-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: cUnknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Peptide
| COCATION: 1..129
| OTHER INFORMATION: /note= "TRT motifs from human"
US-08-854-050-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cech, Thomas R.

APPLICANT: Cech, Thomas R.

Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.

Morlin, Gregg B.

Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: No. 6309867el Telomerase
PRIOR APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 5:36
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 01-OCT-1996
CLASSIFICATION: 5:36
ATTORNEY/AGENT INFORMATION:
NAME: APPLE,
REGISTRATION NUMBER: 015389-002930US
FERENCE/COCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
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PAPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 67, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
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Andrews, William H.
Andrews, William H.
FENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND /ENTION: THERAPEUTIC METHODS
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CTHER INFORMATION: /note= "protein encoded by clone 712562"
US-08-974-549A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 95.4%; Score 145; DB 3; Length 259; Best Local Similarity 93.3%; Pred. No. 2.3e-14; Matches 28; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REPERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acids
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-AFR-1997
FILING DATE: 18-AFR-1997
PRIOR APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-AFR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 05-AFR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 05-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NUMBE: APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
NUMBER: 01-OCT-1997
NUMB
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Patent No. 647579
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Greeg B.
APPLICANT: Morin, Greeg B.
APPLICANT: Harley, Calvin R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Harley, Ca
APPLICANT: Andrews, W
TITLE OF INVENTION: H
TITLE OF INVENTION: T
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-912-951-10
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APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Moxin, Karen B.
APPLICANT: Moxin, Karen B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCE: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two madercadero Center, Eighth Floor
CITY: San Francisco
STREE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 95.4%; Score 145; DB 4; Length 129; Best Local Similarity 93.3%; Pred. No. 1.1e-14; Matches 28; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
US-08-912-951-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: '25-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 10-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION: 435
ATTORNEY ABORN INCOMMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 LFFYRKSVWSKLQSIGIRQHLKRVQLRELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 10, Application US/08974549A; Patent No. 6166178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-974-549A-10
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/note= "63 kDa telomerase protein
encoded by ORF of EcoRI-No. 60938091 insert of
clone 712562"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
CLASSIFICATION:
BRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/74,643
FILING DATE: 10-OCT-1996
CLASSIFICATION:
ATPORMEY/AGENT INFORMATION:
ATPOREY/AGENT INFORMATION:
NAME: APPLICATION NUMBER: 36,429
REBERRICE/OCKET NUMBER: 36,429
REPERRICE/OCKET NUMBER: 36,420
REPERRICE/OCKET NUMBER: 36,420
RELEPHANT: AFG-0300
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH - 564 amino acids
                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
         APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Marley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CAURESPONDENCE ALDERSS:
ADDRESSEE: Townsend and Townsend and Crew I
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                                                                                                                                                                                                                                                                                                                  STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 267, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 564 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein
LOCATION: 1.564
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-08-974-549A-267
                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111
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; OTHER INFORMATION: /note= "protein encoded by clone 712562"
US-08-912-951-10
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                                                                                                                                                             COMPUTER LOUITED SCACUED OL AMMELLE
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 18 PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 09-MAY-1997
CLASSIFICATION NUMBER: US 08/854,050
FILING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 12-APR 1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 12-APR 1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: 015389-002600US
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: 015389-00260US
FILING DATE: 01-OCT-1996
CLASSIFICATION OF SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acide
STRANDENSS:
TELEGRANDENSS:
TELEGRANDENSS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein FEATURE:
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US-08-854-050-101
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encoded by ORF of EcoRI-No. 61661781 insert of
clone 712562"
                  APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: ELOPPY disk
COMPUTER: IEM PC. Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-007-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-ARR-1997
FILING DATE: 18-ARR-1997
FILING DATE: 25-ARR-1997
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA: 08/851,843
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA: 08/851,843
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/915,503
FILING DATE: 10-007-1997
ATORNEY/AGENT INFORMATION:
NAME: APPLICATION NUMBER: 015389-002610US
TELECROMUNICATION NUMBER: 015389-002610US
TELECOMMUNICATION NUMBER: 015389-002610US
TELECOMMUNICATION NUMBER: 015389-002610US
TELECOMMUNICATION NUMBER: 0155000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 267:
SEQUENCE CHARACTERISTICS:
LENGTH: 564 amino acids
TYPE: amino acid
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
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COTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-08-974-549A-267
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Oursy Vacch Similarity 95.4% Score 145, m3.1, Length 564, Matches 35, Conservative 2, Minmatches 0, Indels 0, daps 0, and the conservative 2, Minmatches 0, Indels 0, daps 0, manual and the conservative 2, Minmatches 0, Indels 0, daps 0, manual and the conservative 2, Minmatches 0, Indels 0, daps 0, and the conservative 2, Minmatches 0, Indels 0, daps 0, and the conservative 2, Minmatches 0, Indels 0, daps 0, and the conservative 2, Minmatches 0, Indels 0, daps 0, da
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us-08-854-050-116.rai

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  /note= "63 kDa telomerase protein encoded by ORF of EcoRI-No. 62618361 insert of clone 712562"
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OTHER INFORMATION: /note= "63 kDa telomerase protein
                                                                                                                       Query Match 95.4%; Score 145; DB 3; Length 564; Best Local Similarity 93.3%; Pred. No. 5.6e-14; Matches 28; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTY: California States of America ZIP: 94111
COUNTYER READABLE FORM:
MEDDIUM TYBE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OMPERATION SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION NUMBER: US 08/854,050
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Greeg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                             1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
                                                                                                                                                                                                                                                            25 LFFYRKSVWSKLQSIGIRQHLKRVQLRELS 54
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TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 101, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 564 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Protein
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) OTHER INFORMATION:

) OTHER INFORMATION:

) OTHER INFORMATION:

US-08-854-050-101
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2, Appli
31, Appl
225, App
2, Appli
57, Appl
225, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chaman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020164786A1e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER REACASE FORM:

COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-APP-2001
CLASSIFTCATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend and Crew STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California COUNTRY: United States of America ZIP: 94111
US-10-044-539-10
US-10-282-960-3
US-10-294-778-2
US-10-294-778-10
US-10-294-778-10
US-09-766-253-101
US-09-766-253-101
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US-10-054-611-101
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US-09-900-080-2
US-09-900-080-2
US-10-054-295-225
US-10-295-681-57
US-10-295-225
                                                                                                                                                                                                                                                                                                                                                     US-10-054-611-225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 116, Application US/09843676
Patent No. US20020164786A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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1003
1003
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11132
11132
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  US-09-843-676-116
  Appl
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                                                                                    November 12, 2003, 19:47:20 ; Search time 23.9623 Seconds (without alignments) 215.025 Million cell updates/sec
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Sequence 116, A
Sequence 116, A
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Sequence 116, P
Sequence 116, P
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Sequence 67, 1
Sequence 67, 1
Sequence 67, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
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            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-766-253-116
US-10-053-758-116
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US-10-054-611-67
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US-10-044-692-13
US-10-044-692-13
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152
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                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                      Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length
                                                                                                                                                                                          BLOSUM62
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                                                                                                                                                                                            Scoring table:
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                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                       Run on:
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No.
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Length 30;
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APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US20030009019A1el Telomerase
UNDER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
CLASSIFICATION S36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NAMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION S36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 08/724,643
FILING DATE: US-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 08/724,643
                                                                                                                                    100.0%; Score 152; DB 10; 100.0%; Pred. No. 1.5e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                            1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
                        TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 116:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: California
COUNTRY: United States of America
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 116, Application US/09438486; Publication No. US20030009019A1 GENERAL INFORMATION:
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
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NAME: Apple, Randolph T
REGISTRATION NUMBER: 36,
                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 30; Conservative
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TYPE: amino acid
STRANDEDNESS:
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US-09-766-253-116
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APPLICANT:
APPLICANT:
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FLING DATE: 19-40an-2001
CLASSIFICATION NUMBER: 08/446,017
APPLICATION NUMBER: 08/446,017
FILING DATE: 19-704-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-071-1996
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Andrews, William H.
TITLE OF INVENTION: No. US20020187471A1el Telomerase
NUMBER OF SEQUENCES: 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                               ATTORNAL / ANGRA AN EXPLOSATION TO REGISTRATION NUMBER: 36,429
REFERENCE/FOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 aning acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 152; DB 10; Best Local Similarity 100.0%; Pred. No. 1.5e-15; Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: peptide ; SEQUENCE DESCRIPTION: SEQ ID NO: 116: 18-09-843-676-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
US-09-766-253-116
US-09-766-253-116
Sequence 116, Application US/09766253
Publication No. US20020187471A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Morin, Gregg B.
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  FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                          ATTORNEY/AGENT INFORMATION
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Andrews, William H.
INVENTION: No. US20030044953Alel Telomerase
F. SEQUENCES: 225
         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend and Crew STREET: Two Embarcadero Center, 8th Floor
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100.0%; Pred. No. 1.5e-15;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
      0; Mismatches
                                                  1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
                                                                           1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
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FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-10-054-295-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/854,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                   Sequence 116, Application US/10054295
Publication No. US20030044953A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                   Cech, Thomas R.
Lingner, Joachim
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Chapman, Karen B.
Morin, Gregg B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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INFORMATION FOR SEO ID NO: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94111
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPOLOGY: linear
      30; Conservative
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Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                            US-10-054-295-116
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      Matches
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                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Andrews, William H.
TITLE OF INVENTION: No. US20030032075A1el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                      Query Match

100.0%; Score 152; DB 11;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 015389-002930US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 152; DB 15;
Pred. No. 1.5e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
PAPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
                                                                                                                                                                               1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
                                                                                                                                                                                                                     1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-10-053-758-116
                                                                                                                                                                                                                                                                                                                           Sequence 116, Application US/10053758
Publication No. US20030032075A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94111
COMPUTER READABLE FORM:
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-438-486-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1.129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                   STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PROPER PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morin, Gregg B.
Harley, Calvin
Andrews, Mulliam H.
TITLE OF INVENTION: No. US20020187471A1el Telomerase
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                                         Andrews, William H.
INVENTION: No. US20020164786Alel Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                  NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 01-OCT-1996
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TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 67, Application US/09766253
Publication No. US20020187471A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakamura, Toru
Chapman, Karen B
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                                                                                                                                                                                  CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -09-766-253-67
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                                                                                                                                                                                                                              Andrews, William H.
TITLE OF INVENTION: No. US20030059787A1el Telomerase
NUMBER OF SEQUENCES: 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                             STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
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SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-10-054-611-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/854,050
                   Sequence 116, Application US/10054611 Publication No. US20030059787A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                  APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakamura, Toru
Chapman, Karen B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111
US-10-054-611-116
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Length 129;
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Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030032075Alel Telomerase
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
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COCATION: 1..129

COTHER INFORMATION: /note= "TRT motifs from human"

US-09-438-486-67
                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 12-NOV-1999
CLASSIFICATION: 536
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Pred. No. 7.7e-14;
2; Mismatches 0;
                                                                                                                                                            FILING DATE: 12-NOV-1999
CLASSIFICATION NOMER: 05/91999
CLASSIFICATION DATA:
APPLICATION NUMBER: 05/981,843
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 05/9846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: 05/9844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: 05/9844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: 05/987
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: 05/987
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 015389-002931US
TELEPHONE: (415) 576-0200
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Publication No. US20030032075A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 576-0200 TELEPAX: (415) 576-0200 INFORMATION FOR SEQ ID NO: 67 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 93.3%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-053-758-67
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Pred. No. 7.7e-14;
                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPATER: PLOPPY Group COMPATIONE
CORPARING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: CURROWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1.7129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
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          CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
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APPLICANT: Lingner, Joachim
APPLICANT: Lingmer, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Andrews, William H.
APPLICANT: Andrews, William H.
ANDRER OF SEQUENCES: 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 95.4%; Score 145; DB Best Local Similarity 93.3%; Pred. No. 7.7e Matches 28; Conservative 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 576-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: 1..129
; SEQUENCE DESCRIPTION: /note= "TRT motifs from human"
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andrews, William H.
TITLE OF INVENTION: No. US20030059787A1el Telomerase
NUMBER OF SEQUENCES: 225
                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
CARDESPEE: Townsend and Townsend and Crew
ADDRESSEE: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REGISTRATION INDRER: 36,429
TELECEMONER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 145; DB 15;
Pred. No. 7.7e-14;
2; Mismatches 0;
                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
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COUNTRY: United States of America
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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Publication No. US20030059787A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: <Unknown>
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Chapman, Karen B.
Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 67
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 93.3 Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-054-611-67
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APPLICANT: Cech, Thomas R.
Lingmar, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. US20030044953A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: /note= "TRT motife from human" SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                              MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
95.4%; Score 145; DB 15;
Best Local Similarity 93.3%; Pred. No. 7.7e-14;
Matches 28; Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
PAPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
                                                                                                                                                                                                                                                                                                                                                                                      PILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
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COUNTRY: United States of America
ZIP: 94111
  COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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Publication No. US20030044953A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 67:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1..129
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                          ZIP: 94111
COMPUTER READABLE FORM:
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Lingner, Joachim
Nakamura, Toru
Chapmar, Aren B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                  FILING DATE: «UNKNOWN)

PELLING DATE: «UNKNOWN)

PELLING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-ARP-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

APPLICATION NUMBER: US 08/724,643

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/ACENT INFORMATION:

NAME: APPL SANGOLD TO TELEPRAX: (415) 576-0200

TELEPRAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 129 amino acids

LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 145; DB 15;
Pred. No. 7.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
95.4%; Score 145; DE
Best Local Similarity 93.3%; Pred. No. 7.7e
Matches 28; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
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                                                                          APPLICATION NUMBER: 08/912,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/10044539
Publication No. US20030100093A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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OTHER INFORMATION:
                                                    PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1.7129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREBT: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                          PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 08/854,050

FILING DATE: c10known
APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

REGISTATION NUMBER: 36,429

REGISTATION NUMBER: 36,429

REGISTATION NUMBER: 36,429

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LFFYRKSVWSKLOSIGIROHLKRVOLRDVS 30
                 ENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
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APPLICATION NUMBER: US/10/044,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/10044692;
Publication No. US20030096344A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 576-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEO ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: <Unknown>
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Best Local Similarity
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                      CURRENT
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CURRENT APPLICATION DATA
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Best Local Similarity
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Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMBRASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPBUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: /note= "TRT motifs from human" SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOPEMING SYSTEM: PC-DOS/MS-DOS
OPFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REBERBNCFJOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951

FILING DATE: «Unknown:
APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 15-APP-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18 APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 10-CT-1996

ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
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Publication No. US20030096344A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                         FILING DATE: 11-Jan-2002
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: peptide
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LOCATION: 1..259
OTHER INFORMATION: /note= "protein encoded by clone 712562"
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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                                                                                                                                                                                                                                                                                                                                                             NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 145; DB 15;
Pred. No. 1.6e-13;
                                                                                     FILING DATE: CURRICOND
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 LFFYRKSVWSKLÓSIGIRQHLKRVQLRELS 54
                                               PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/912,951
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 259 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 576-(
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5h 95.4%;
I Similarity 93.3%;
28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
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Search completed: November 12, 2003, 19:55:47 Job time : 23.9623 secs

Perfect score:

Title:

9

Run

Sequence:

Scoring table:

Searched:

Database

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N'Alternate names: telomerase reverse transcriptase
C'Species: Homo sapiens (man)
C'Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C'Accession: T03844
R'Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J
R'Aitle: Telomerase catalytic subunit homologs from fission yeast and human.
A'Ritle: Telomerase catalytic subunit homologs from fission yeast and human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cispecies: Oxytricha trifallax
Cispecies: Oxytricha trifallax
Cispecies: Oxytricha trifallax
Cibate: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
CiAccession: T31107
RiBryan, T.M.; Sperger, J.M.; Chapman, K.B.; Cech, T.R.
RiBryan, T.M.; Sperger, J.S.A. 95, 8479-8484, 1999
A;Title: Telomerase reverse transcriptase genes in Tetrahymena thermophila and Oxytrich
A;Reference number: 220985; MUID:98337940; PMID:9671703
                                                                                              hypothetical proce
probable acetyltra
conserved hypothet
NADH2 dehydrogenas
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1132 <NAK>
A;Cross-references: EMBL,AF015950; NID:g2330016; PIDN:AAC51672.1; PID:g2330017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-1132 <BRY>
A;Gross-references: EMBL:AF060230; NID:g3342795; PID:g3342796; PIDN:AAC39163.1
C;Genetics:
               probable integrase
iron(III) dicitrat
                                                      hypothetical prote
NADH dehydrogenase
Delta8 sphingolipi
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protein-tyrosine k
 hypothetical prote
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                                        peroxidase (EC 1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 42.8%; Score 65; DB 2; Length 1132; Best Local Similarity 30.3%; Pred. No. 0.32; Matches 10; Conservative 14; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: T31107
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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C65002
A71332
AC2421
S55035
T16883
D90175
S63159
AG0371
T139744
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S23065
A41527
                                                                                                                                                  A59433
TVFF7L
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306
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898
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Les 28; Conser
A; Accession: T03844
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Query Match
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Matches
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apolipoprotein B-1
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                                                                                       2003, 19:43:04; Search time 11.6981 Seconds (without alignments) 246.626 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PET309 protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                           1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                              283308 segs, 96168682 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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S48988
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LPHUB
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F85069
S64249
T14891
S58393
AI3168
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AF1520
T40697
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T39572
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G82735
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B70044
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SYBYMX
MNWVRA
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                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                               US-08-854-050-116
152
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Match Length
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958
11117
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72
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234
281
                                                                                           November 12,
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1: pir1:*
2: pir2:*
3: pir3:*
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Score

Result No.

51.5 50.5 50.5 50.5 50.5

48 47.5 47

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us-08-854-050-116.rpr

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R;Pape, M.E.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-526 <MAC>
A;Cross-references: EMBL:U00029; NID:g551322; PID:g458924; GSPDB:GN00008; MIPS:YHR207c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: GB:U67549; GB:L77117; NID:92826363; PIDN:AAB99062.1; PID:91591711;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein YHR207c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 19-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              apolipoprotein B - crab-eating macaque (fragment)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 13-Aug-1999
C;Accession: S32802
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                            Indels
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A, Description: The sequence of S. cerevisiae cosmid 9177.
A, Reference number: $46671
A, Accession: $48988
A, Molecule type: DNA
                            7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LFFYR-KSVWSKLQSIGIRQHLKRVQLRDVS 30
Pred. No. 58;
2; Mismatches
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35.5%; Pred. No. 16;
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48.0%; Pred. No. 19;
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                                                                               3 FYRKSVWSKLOSIGIROHLK 22
  55.0%;
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A;Cross-references: SGD:S0001250
A;Map position: 8R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: FOR997396-999225
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R; Macri, C.
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A; Residues: 1-2479 «FAR»
C; Comment: Readthrough of the terminator codon UGA occurs between the codons UUC for 186
C; Superfamily: Semliki Forest virus nonstructural protein
C; Keywords: nonstructural protein; polyprotein
F; 1-533 Product: nonstructural protein NS1 #status predicted <NS2>
F; 1332-1868/Product: nonstructural protein NS2 #status predicted <NS3>
F; 1869-2479/Product: nonstructural protein NS4 #status predicted <NS3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: GB:X12864; NID:g4839; PIDN:CAA31343.1; PID:g4842
A,Cross-references: GB:X12864; NID:g4839; PIDN:CAA31343.1; PID:g4842
A,Note: the Source is designated as Saccharomyces douglasii
R;Herbert, C.J.; Labouesse, M.; Dujardin, G.; Slonimski, P.P.
EMBO J. 7, 473-483, 1988
A,Title: The NAM2 proteins from S.cerevisiae and S.douglasii are mitochondrial leucyl-tR
A,Reference number: S00341; MUID:88211560; PMID:3284745
A,Accession: S00341
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R;Faragher, S.G; Meek, A.D.J.; Rice, C.M.; Dalgarno, L.
Rivology, 163, 509-526, 1988
A;Title: Genome sequences of a mouse-avirulent and a mouse-virulent strain of Ross River
A;Reference number: A94373; MUID:88179556; PMID:2833022
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C;Superfamily: leucine-tRNA ligase
C;Superfamily: leucine-tRNA synthetase; ATP; ligase; mitochondrion; protein biosynthesis;
C;Superfamily: ransit peptide (mitochondrion) #status predicted <TNP>
F;1-48/Domain: transit peptide (mitochondrion) #status predicted <MAT>
F;49-894/Product: leucine-tRNA ligase #status predicted <MAT>
F;63-66/Region: ATP binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nonstructural polyprotein - Ross River virus (strain NB5092 mouse-avirulent)
NSContains: nonstructural protein NS1; nonstructural protein NS2; nonstructural protein C;Species: Ross River virus
C;Species: Ross River virus
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 12-Jun-1998
                                                                                                                                                                                  Outcine-tRNA ligase (EC 6.1.1.4) precursor, mitochondrial - yeast (Saccharomyces sp.) NyAlternate names: leucyl-tRNA synthetase (Saccharomyces sp.) NyAlternate names: leucyl-tRNA synthetase (Spechase Saccharomyces sp.) Outcisses Saccharomyces sp. (Spechase Saccharomyces sp.) Saccharomyces sp. (Spacession: S18754; S00341

Riherbert, C.J.; Dujardin, G.; Labouesse, M.; Slonimski, P.P.
Mol. Gen. Genet. 213, 297-309, 1988
A;Title: Divergence of the mitochondrial leucyl tRNA synthetase genes in two closely sp. A;Reference number: S18752; MUID:89039717; PMID:3054483
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A;Residues: 26-894 <HER2>
A;Note: the source is designated as Saccharomyces douglasii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
20;
                               1 LFFYRKSVWSKLQSIGI ----RQHLKRVQLRDV 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1350-369/Region: zinc finger CHCH motif
1462-506/Region: zinc finger CCCC motif
1628-632/Region: tRNA binding #status predicted
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421 RKSIMGKLHSKGLSKNIIRYRIRD 444
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Best Local Similarity 41.73
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-894 <HER1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
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A;Reference number: A24320; MUID:86287319; PMID:3461454
A;Accession: A24320
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A;Accession: A24320
A;Accession: A24320
A;Residues: 1-97,'I',99-617,'A',619-941,'YYIWSLPPRP,',951-1138,'PTGRLPNCFSNGLICYSLWLHSFQ
A;Residues: 1-97,'I',99-617,'A',619-941,'YYIWSLPPRP,',951-1138,'PTGRLPNCFSNGLICYSLWLHSFQ
A;Residues: 1-97,'I',99-617,'A',HOSP31, ND:317821,'PID:353189
B;Cros. Teferences: Galwidge, A.Y.; Anchors, J.M.; Sakaguchi, A.Y.; Naylor,
Britue: Muman apolipoprotein B-100: cloning, analysis of liver mRNA, and assignment of
A;Reference number: A24684; MUID:86094221; PMID:3001697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA

A; Residues: 485-617, A', 619-1044 <LA2>

A; Cross-references: GB:M12480; NID:g178791; PIDN: AAA51751.1; PID:g178792

B; Procter, A.A.; Hardman, D.A.; Schilling, J.W.; Miller, J.; Appleby, V.; Chen, G.C.; K

Proc. Natl. Acad. Sci. U.S.A. 83, 1467-1471, 1986

A; Pitle: Isolation of a cDNA clone encoding the amino-terminal region of human apolipop

A; Reference number: A94088; MUID: 86149325; PMID: 3513177
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A; Accession: A56533
A; Molecule type: mRNA
A; Residues: 1282-2721, 742-3290, 'L', 3292-3336, 'N', 3338-3948,'F', 3950-3963,'Y', 3965-4180
A; Cross-references: GB:M15421; NID:9178817; PIDN:AAA51758.1; PID:9178818
B; Article: Structural comparison of human apolipoproteins B-48 and B-100.
A; Reference number: A29671; MUID:88050832; PMID:3676265
A; Accession: A29671
A; Reference number: A29671; MUID:88050832; PMID:3676265
A; Accession: A29671
A; Residues: 1671-2323, 'PW', 2327-2352,'H', 2354-2398 cHAR>
A; Residues: 1671-2323, 'PW', 2327-2352,'H', 2354-2398 cHAR>
A; Residues: 1671-2323, 'PW', 2327-2352,'H', 2354-2398 cHAR>
A; Rosidues: 1671-2323, 'RW', 2327-2352, 'RW', 2344-1481
A; Rosidues: 1671-2323, 'RW', 2327-2352, 'RW', 2354-2398 cHAR>
A; Rosidues: 1671-2323, 'RW', 2327-2352, 'RW', 2354-2398 cHAR>
A; Rosidues: 1671-2323, 'RW', 2327-2352, 'RW', 2354-2398 cHAR>
A; Rosidues: 3846-4298 cHOS
A; Rosidues: 4219-4377, 'R', 4339-4563 cPFI>
A; Rosidues: 4219-4377, 'R', 4339-4564 cPFI>
A; Rosidues: 4219-4419, A; A; A; A; A; A
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A; Residues: 'N', 3729-371,'I', 3733-3875,'A', 3877-3948,'F', 3950-3963,'Y', 3965-3982,'S', 3
A; Cross -references: GB:M12413; NID:g178735; PIDN:AAA51742.1; PID:g178736
A; Chen, S.H.; Habib, G.; Yang, C.Y.; Gu, Z.W.; Lee, B.R.; Weng, S.; Silberman, S.R.; Ca
Science 238, 363-366, 1987
A; Title: Apolipoprotein B-48 is the product of a messenger RNA with an organ-specific i
A; Reference number: A40133; MUID:88018019; PMID:3659919
A; Molecule type: mRNA
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A,Molecule type: MRA
A,Molecule type: MRA
A,Residues: 709-791, 'SSSWKAASHGCPHSAGD',810-906 <DEE>
A,Residues: 709-791, 'SSSWKAASHGCPHSAGD',810-906 <DEE>
A,Cross-references: GB:K03175; NID:gJ78821, PIDN:AAA51759.1; PID:gJ78822
A,Cross-references: GB:K03175; NID:gJ78821, PIDN:AAA51759.1; PID:gJ78822
GGne 49, 29-51, 1986
A,Title: Analysis of the human apolipoprotein B gene; complete structure of A,Reference number: A91565; MUID:87191999; PMID:2883086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Cross-references: GB:M12681; NID:g178797; PIDN:AAA51753.1; PID:g178798 R; Deeb, S.S.; Motulsky, A.G.; Albers, J.J.
Rr, Deeb, S.S.; Motulsky, A.G.; Albers, J.J.
Rr, Deeb, S.S.; Motulsky, A.G.; Albers, J.J.
A, Title: A partial cDNA clone for human apoliprocein B.
A; Reference number: A25774; MUID:85270450; PMID:3860836
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A;Residues: 1-291 <PRO>
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N.Contains: apolipoprotein B-26; apolipoprotein B-48; apolipoprotein B-74
C.Species: Homo sapiens (man)
C.Species: B-Dec-1987 #Sequence_revision 28-Dec-1987 #text change 21-Jul-2000
C.Species: 28-Dec-1987 #Sequence_revision 28-Dec-1987 #text change 21-Jul-2000
C.Species: 28-Dec-1987 #Sequence_revision 28-Dec-1987 #text change 21-Jul-2000
C.Speciesion: AZ7850; AZ5679; AZ5263; A25265; AZ5266; AZ4620; AZ4684; AZ3817; AZ5774; AZ6
R.S.Ludwig, E.H.: Blackhart, B.D.; Pierotti, V.R.; Calati, L.; Fortier, C.; Knott, T.; Scc
DNA 6, 363-372, 1987
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A; Residues: 1-97, I', 99-328, V', 330-644, I', 646-918, P', 920-3318, D', 3320-3426, T', 3428-
A; Residues: 1-97, I', 1418-4180, E', 4182-4563 - CHES.
A; Cross-references: GB: J02610; NID: 9178803; PIDN: AAA35549.1; PID: 9178804
A; Note: a total of 2366 residues were confirmed by direct sequencing of tryptic peptides
R; Protter, A.A.; Hardman, D.A.; Sato, K.Y.; Schilling, J.W.; Yamanaka, M.; Hort, Y.J.; H
Proc. Natl. Acad. Sci. U.S.A. 83, 5678-5682, 1986
A; Title: Analysis of cDNA clones encoding the entire B-26 region of human apolipoprotein
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A; Residues: 1-272, N', 274-617,'A', 619-1217,'E', 1219-2091,'V',2093-2364,'T',2366-2679,'Q'
A; Cross-references: GB:X04506; NID:g34330; PIDN:CAA28191.1; PID:g3431
B; Law, S.W.; Grant, S.M.; Higuchi, K.; Hospettankar, A.; Lackner, K.; Lee, N.; Brewer Jr
Proc. Natl. Acad. Sci. U.S.A. 83, 8142-8146, 1986
A; Titles Human liver apolipoprotein B-100 cDNA: complete nucleic acid and derived amino
A; Reference number: A94134; MUID:87041416; PMID:3464946
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A; Residues: 1-617, 'A', 619-703,'P', 705-792,'R', 794-1270,'S', 1272-1866,'G', 1868-2036,'N', 2
4189-4220,'M', 4222-4563 «LAW>
4180-4220,'M', 4222-4563 «LAW>
A; Note: the codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and
B; Chen, S.H.; Yang, C.Y.; Chen, P.F.; Setzer, D.; Tanimura, M.; Li, W.H.; Gotto Jr., A.M
J. Biol. Chem. 261, 12918-12921, 1986
A; Title: The complete cDNA and amino acid sequence of human apolipoprotein B-100.
A; Reference number: A92556; MUID: 87008488; PMID: 3759943
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A,Residues: 1-617,'A',619-1929,'F',1931-3318,'D',3320-3426,'T',3428-3431,'Q',3433-3731,'A',Cross-references: GB:M14162
A;Cross-references: GB:M14162
R;Cladaras, C.; Hadzopoulou-Cladaras, M.; Nolte, R.T.; Atkinson, D.; Zannis, V.I.
EMBO J. 5, 3495-3507, 1986
A;Title: The complete sequence and structural analysis of human apolipoprotein B-100: r'A;Reference number: A91058; MUID:87161758; PMID:3030729
Biochim. Biophys. Acta 1086, 326-334, 1991
A;Title: Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional
A;Reference number: S32802; MUID:92075708; PMID:1742325
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A; Residues: 1-11,15-2539,'S',2541-3823,'R',3825-4563 <CLA>
A; Residues: 1-109-Asp was also found
R; Knott: 1.03-Asp was also found
Nucleic Acids Res. 14, 7501-7503, 1986
A; Title: Complete cDNA and derived protein sequence of human apolipoprotein B-100.
A; Reference number: A93639; MUID:87016385; PMID:3763409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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A;Molecule type: mRNA
A;Residues: 1-508 cAPA>
A;Cross-references: EMBL:X15737; NID:g38047; PIDN:CAA33755.1; PID:g930126
C;Superfamily: apolipoprocein B
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A;Reference number: A27850; MUID:88003974; PMID:3652907
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Pred. No. 22;
3; Mismatches
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50.0%;
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Best Local Similarity 50.09
Marches 12; Conservative
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hypothetical protein F11C1.190 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Space: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000 (Spacession: T45581 (Spacession: T45581 (Spacesyles, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; Masubmitted to the Protein Sequence Database, December 1999
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R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschi A;Reference number: A64300; MUID:96337999; PMID:8688087
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A,Title: Apolipoprotein B is a calcium binding protein.
A,Reference number: A90125; MUD:86542245; PMID:3087360
A,Contents: annotation; Calcium binding
R;Carlsson, P:, Olofeson, S.O.; Bondjers, G.; Darnfors, C.; Wiklund, O.; Bjursell, Wicleic Acids Res. 13, 8813-8826, 1985
A,Title: Molecular cloning of human apolipoprotein B cDNA.
A,Reference number: 137178; MUD:86093680; PMID:3841204
A,Recession: 137180
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C,Species: Methanococcus jannaschii
C,Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                     Length 4563;
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Pred. No. 9.2;
6; Mismatches 1; Indels
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A,Experimental source: cultivar Columbia; BAC clone F11C1
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Pred. No. 1.8e+02;
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Pred. No. 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3680 YDKSLWDFLKLDVTTSIGRROHLR 3703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 YRKSVWSKLQ----SIGIROHLK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 RKSVWSKLOSIGIROHLKR 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 REEAWSKRÓDISRHRHLRR 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.9%;
53.3%;
                                                                                                                                                                                                                                                                                                                     33.2%;
50.0%;
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                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.v.
12; Conservative
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Best Local Similarity 47.4%
Local Similarity 47.4%
Conservative
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Best Local Similarity 53.3
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Accession: T45581
A, Status: preliminary
A, Molecule type: DNA
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A;Introns: 9/1; 148/1
A;Note: F11C1.190
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A; Residues: 2169-2179 <hOS>
A; Note: the sequence shown represents the carboxyl end of apolipoprotein B-48
A; Note: two RNA species, 14.1kb and 7.5kb in length, were isolated from the human intest
chencodes the 250K apo8-48, CAA encoding 2180-Gin is substituted by the stop codon TAA,
R; Yang, C; Kim, T.W.; Weng, S; Lee, B; Yang, M; Gotto Jr., A.M.
R; Yang, Cs, Kim, T.W.; Weng, S; Lee, B; Yang, M; Gotto Jr., A.M.
A; Title: Isolation and characterization of sulfhydryl and disulfide peptides of human ap
A; Contents: disulfide bonds
                                                                                                                                               A; Molecule type: protein
A; Residues: 51-75;101-110;129-139;158-174;197-207;276-287;298-304;306-314;526-532;538-55
A; 1486-1498;1537-1556;1563-1572;1601-1610;1647-1661;1697-1724;1770-1781;1859-1897;1968-
A; Note: these fragments were derived from apo48
B; Hardman, D.A.; Protter, A.A.; Schilling, J.W.; Kane, J.P.
Biochem. B; Diophys. Res. Commun. 149, 1214-1219, 1987
A; Title: Carboxyt terminal analysis of human B-48 protein confirms the novel mechanism p
A; Reference number: A28002; MUID:88106542; PMID:3426612
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A;Title: Human apolipoprotein B: partial amino acid sequence.
A;Reference number: A22006; MUID:84208786; PMID:6373369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 28-41;76-97,'I',99-100;175-193;206-215;239-249;259-266;357-399;455-490;512-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: mRNA
A,Residues: 3056-3159 «MEH»
A,Crosa-references: GB:X03045; NID:g28783; PIDN:CAA26850.1; PID:g929609
A,Crosa-references: GB:X03045; NID:g28783; PIDN:CAA26850.1; PID:g929609
R;Hospattankar, A.V.; Higuchi, K.; Law, S.W.; Meglin, N.; Brewer Jr., H.B.
Biochem. Biophys: Res. Commun. 148, 279-285, 1987
A;Title: Identification of a novel in-frame translational stop codon in human intestine
A;Reference number: A29659; MUID:88049670; PMID:2445342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Experimental source: intestine A, Experimental source: intestine A, Note: this mRNA from intestine includes a stop codon created by RNA editing in place A, Note: this mRNA from intestine includes G.C.; West, R.; Johnson, D.F.; Kirchgessner, Nucleic Acids Res. 13, 6917-6953, 1985
A, Title: Human apolipoprotein B: identification of cDNA clones and characterization of A, Reference number: A24269; MUID:86041888; PMID:3903660
                                              A;Cross-references: GB:M18036; NID:g178799; PIDN:AAA51754.1; PID:g178800 A;Note: this mRNA includes the stop codon of the organ-specific mRNA for apo48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Contents: annotation; gene structure
R;Weisgraber, K.H.; Rall Jr., S.C.
J. Biol. Chem. 262, 11097-11103, 1987
A;Title: Human apolipoprotein B-100 heparin-binding sites.
A;Reference number: A92605, MUID: 87280197; PMID: 3301850
A;Contents: annotation; heparin binding and disulfide bond
R;Dashti, N.; Lee, D.M.; Mok, T.
Biochem. Biophys. Res. Commun. 137, 493-499, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 2129-2179,2181-2235 <HA2>
A;Cross-references: GB:M18471
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A;Accession: S64249
A;Molecule type: DNA
A;Reidues: 1-958 <FRR>
A;Residues: 1-958 <FRR>
A;Cross-references: EMBL:Z72749; NID:g1322880; PIDN:CAA96943.1; PID:e243888; PID:g13228°
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: T14891
R;Collins, K.; Gandhi, L.
R;Collins, K.; Gandhi, L.
R;Collins, K.; Gandhi, L.
A;Title: The reverse transcriptase component of the Tetrahymena telomerase ribonucleopric A;Reference number: Z18252; MUID:98337941; PMID:9671704
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N;Alternate names: protein L2189; protein YLR067c
C;Species Saccharomyces cerevisiae
C;Date: 29-Nov-1995 #sequence revision 12-Apr-1996 #text_change 07-May-1999
C;Accession: S58393; S61640; S30879; S64895; S64899
EMBO J. 14, 4031-4043, 1995
A;Title: The product of the nuclear gene PET309 is required for translation of mature m.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: S58393; MUID:95393979; PMID:7664742
A;Accession: S58393
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-965 < MAN>
A;Cross-references: EMBL:L06072; NID:g172129; PID:g172130
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  telomerase (BC 2.7.7.-) catalytic chain pl13 - Tetrahymena thermophila N;Alternate names: telomerase reverse transcriptase C;Species: Tetrahymena thermophila C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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A;Molecule type: mRNA
A;Residues: 1-1117 <COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                Score 49; DB 2
Pred. No. 59;
4; Mismatches
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A;Map position: 7L
C;Superfamily: WW repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                32.2%;
53.8%;
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Best Local Similarity 53 ...,
A: Conservative
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Best Local Similarity 34.54
Matches 10; Conservative
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A;Gene: TERT
A;Genetic code: SGC5
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                                                                                                                                                                                                                                       A, Gene: SGD:TIN1
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                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: AD2061
R;Kancko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaiki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: F85069
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprint Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: F8506
A;Accession: F8506
A;Status: preliminary
A;Residues: 1-660 <STO>
                                                                                                                                                                                                                                                     hypothetical protein alr2042 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
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A;Cross-references: GB:BA00019; PIDN:BAB73741.1; PID:g17131133; GSPDB:GN00179
A;Cross-references: strain PCC 7120
C;Genetics: A,Gene: alr2042
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N;Alternate names: hypothetical protein G0958
C;Species: Saccharomyces cerevisiae
C;Species: T1-May-1996 #sequence_revision 17-May-1996 #text_change 29-Oct-1999
C;Accession: S64249
R;Fartmann, B.; Kramer, W.
submitted to the Protein Sequence Database, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein AT4g05540 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb_2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
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2; Mismatches
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                                               Conservative
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Matches 9; Conservative
                  LOSIGIROHLKRVOL
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
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A;Map position: 4
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A;Map position: 12R
C;Keywords transmembrane protein
F;240-256/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                              Sipoli, T.M.

submitted to the Protein Sequence Database, May 1996
A;Reference number: S64899
A;Accession: S64899
A;Accession: S64899
A;Residues: 1-551
A;Residues: 1-551 <POH>
A;Coss-references: EMB1:Z73239; MIPS:YLR067C
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 31.2%; Score 47.5; Di
Best Local Similarity 37.0%; Pred. No. 98;
Matches 10; Conservative 7; Mismatches
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Search completed: November 12, 2003, 19:52:01 Job time : 12.6981 secs

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076372 mus musculu
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P13503 saccharomyc
P13887 ross river
058458 methanococc
938910 saccharomyc
P04114 homo sapien
057639 methanococc
000939 euplotes ae
P53076 saccharomyc
077448 tetrahymena
090416 homo sapien
P57827 pasteurella
P32522 saccharomyc
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P32528 mus musculu
0802b3 mus musculu
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                            US-08-854-050-116
152
1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
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                                                                                                                                   127863 seqs, 47026705 residues
                                                                                                                                                                                                                                                                        SUMMARIES
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OUT2_HUMAN
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YZ04_METUA
YZ04_METUA
YZ04_HUMAN
HDA4_CHICK
HDA4_HUMAN
HDA4_HUMAN
HDA4_HUMAN
HDA5_MOUSE
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UF0_HUMAN
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Maximum Match 100%
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| Qgrf86 fusobacteri P43121 homo sapien P32052 escherichia P44967 haemophilus Q88981 buchnera ap Q89a93 buchnera ap Q9nrj5 homo sapien P41504 rhizobium 1 Q96520 arabidopsis P30000 escherichia Q02151 caenorhabdi Q45436 caenorhabdi | PRT; 1132 AA. sed) sequence update) annotation update) ptase (EC 2.7.7) (Telomerase catalytic | TISSUB=Kidney; MEDLINE=97400623; PubMed=9252327; MEDLINE=97400623; PubMed=9252327; Makamura T.M., Morin G.B., Chapman K.B., Weinrich S.L., Andrews W.H., Lingner J., Harley C.B., Cech T.R.; "Telomerase catalytic subunit homologs from fission yeast and human."; Science 277:955-959(1997). [2] SEQUENCE FROM N.A. MEDLINE=97433088; PubMed=9288757; Meyerson M., Counter C.M., Eaton E.N., Ellisen L.W., Steiner P., Caddle S.D., Zalangra L., Beljersbergen R.L., Davidoff M.J., Liu Q., Bacchetti S., Haber D.A., Weinberg R.A.; Davidoff M.J., Liu Q., "hEST2, the putative human telomerase catalytic subunit gene, is uprequlated in tumor cells and during immortalization."; [3] | SEQUENCE FROM N.A. WICK M., Zubov D., Hagen G.; Wick M., Zubov D., Hagen G.; "Genomic organization and promoter characterization of the gene encoding the human telomerase reverse transcriptase (hTERT) ."; Genocoding the human telomerase reverse transcriptase (hTERT) ."; Genocoding the human telomerase reverse transcriptase (hTERT) ."; [4] ESQUENCE FROM N.A. [54] SEQUENCE FROM N.A. "Sequence of a BAC carrying the entire hTERT gene."; "Sequence of a BAC carrying the entire hTERT gene."; "Sequence of a BAC carrying the ENBLOGNED READSES. "Sequence of a BAC carrying the ENBLOGNED READSES. "Sequence of a BAC carrying the ENBLOGNED READSES. "Sequence of a BAC carrying the ENBLOGNED READSES. IT THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT ELOWEATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME. -! SUBUNIT: Interacts with PINX! -! SUBUNIT: Interacts with PINX! -! SUBUNIT: Interacts with PINX! -! SUBURITY: BELONGE REPEATS -! SIMPLE SEQUENCE REPEATS -! SIMPLE SEQUENCE REPEATS -! SIMPLE SEQUENCE WITHIN THE RUBBERS HANDSCRIPTASE FAMILY. TELOMERASE SUBPAMILY TELOMERASE SUBPAMILY. TELOMERASE SUBPAMILY. TELOMERASE SUBPAMILY. |
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| 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | UMAN ERT HUMA ERT HUMA 1476; 0 0-MAY-20 0-MAY-20 8-FEB-20 8-FEB-20 GET OR T OMO SADIUIT) UNATORE AMMAIIA; | SEQUENCE FROM N.A. TESSUE-Kidney; MEDLINE=97400623; PubMed= Nakamura T.M., Morin G.B. Lingner J., Harley C.B., "Telomerase caralytic sub- Science 277:955-959(1997) [2] SAGUENCE FROM N.A. MEDLINE=9743088; PubMed= Meyerson M., Counter C.M. Gadle S.D., Zlaugra L., Bacchetti S., Haber D.A., "HEST2, the putative human regulated in tumor cells (Cell 90:785-795(1997)). | SEQUENCE FROM N.A. MEDGINES 9267444; Pubmed=10333526; Wick M., Zubov D., Hagen G.; "Genomic organization and promoter characterizati encoding the human telomerase reverse transcripta Gene 232:97-106(1999). [4] SEQUENCE FROM N.A. LONDONO-Vallejo J.A.; "Sequence of a BAC carrying the entire hTERT gene Submitted (OCT-2001) to the EMBL/GenBank/DDBJ dat -! STUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ELONAATES TELOMERASE IT IS A REVERSE TRANSCRI SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZY SIMPLE SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZY SIMPLE ACTIVATION OF TELOMERASE HAS BEEN IM -! SUBCELLULAR LOCATION: Nuclear! DISEASE: ACTIVATION OF TELOMERASE TRANSCRIPT TELOMERASE SUBFAMILY! SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPT TELOMERASE SUBFAMILY |
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SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                   GO; GO:0005696; C:telomere; TAS.
GO; GO:0003721; F:telomeric template RNA reverse transcriptas. . .; TAS.
GO; GO:0007003; P:telomere binding; TAS.
InterPro; IPR000477; RVIse.
InterPro; IPR003545; Telomerase_RT.
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                                                                                                                                                                                                                                                                                                         PRINTS; PR01365; TELOMERASERT.
Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homolog.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL I THE REPLICATION OF CHROWOSME TERMINI IN MOST BUYARYOTES. IT ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS
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MEDLINE=98241176; PubMed=9582020;
Greenberg R.A., Allsopp R.C., Chin L., Morin G.B., DePinho R.A.;
"Expression of mouse telomerase reverse transcriptase during development, differentiation and proliferation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98393668; PubMed=9724727;
Martin-Rivera L., Herrera E., Albar J.P., Blasco M.A.;
"Expression of mouse telomerase catalytic subunit in embryos and adult tissues.";
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Pred. No. 5.9e-14;
2; Mismatches 0; Indels C
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94E35469C4CA33A0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Telomerase reverse transcriptase (EC 2.7.7.-)
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                                                                                                                  EMBL; AF018167; AAC51724.1; -.
EMBL; AF128894; AAD30037.1; -.
EMBL; AF128893; AAD30037.1; JOINED.
EMBL; AY007685; AAC23289.1; -.
                                                                                                                                                                                                                                                                                                                                                    126996 MW;
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070372; 035432;
30-MAX-2000 (Rel. 39, Created)
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Matches 28; Conservative
                                                                                                                                                                     PIR; T03844; T03844.
Genew; HGNC:11730; TERT.
MIM; 187270; -.
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1132 AA; 1
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                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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30-MAY-2000 (Rel. 39, Last annotation update)
Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit) (Telomerase subunit Pl33).
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Stichotrichida, Oxytrichidae, Oxytricha.
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Pred. No. 1.4e-12;
5; Mismatches 0; Indels
SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
SUBUNIT: Interacts with PINX1 (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY. BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
TELOMERASE SUBFAMILY.
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127977 MW; F85266905DD6558C CRC64;
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InterPro; IPR000477; RVTse.
InterPro; IPR00345; Telomerase_RT:
Pfam; PR0078; rvt; 1.
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MEDLINE=98337940; Pubmed=9671703;
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Local Similarity 83.3%;
les 25; Conservative 5
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1122 AA;
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IsoId=Q9UKV0-3; Sequence=VSP_002083, VSP_002084;
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1011 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 437
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"HDAC4, a human histone deacetylase related to yeast HDA1, is a transcriptional corepressor.";

Mol. Cell. Biol. 19:7816-7827(1999).

-! FUNCTION: Responsible for the deacetylation of lysine residues on the N-terminal part of the core histones (H2A, H2B, H3 and H4). Histone deacetylation gives a tag for epigenetic repression and plays an important role in transcriptional regulation, cell cycle progression and developmental events. Histone deacetylases act via the formation of large multiprotein complexes (By similarity).
                                                                                                                                                          Gaps
                                                                       Iransferase; RNA-directed DNA polymerase; Telomere; Muclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N.,
Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XI.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
DNA Res. 5:277-286(1998).
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21438017; PubMed=11535832;
Zhou X., Marks P.A., Rifkind R.A., Richon V.M.;
"Cloning and characterization of a histone deacetylase, HDAC9.";
Proc. Natl. Acad. Sci. U.S.A. 98:10572-10577(2001).
                                                                                                                                                          4
                                                                                                                               Length 1132;
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS 1 AND 4), AND CHARACTERIZATION
                                                                                                                                                          5; Indels
                                                                                                     1132 AA; 134124 MW; 81E145F5F24392DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Nuclear (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=4; Comment=Additional isoforms seem to exist;
                                                                                                                                DB 1;
                                                                                                                                                                                               1 LFFYRKSVWSKLQSIGI----RQHLKRVQLRDV 29
                                                                                                                                                                                                                                                                       HDA9_HUMAN STANDARD; PRT; 1011 AA. Q9UKV0; 094845; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 42, Last annotation update) Histone deacetylase 9 (HD9) (HD7B) (HD7). HDAC9 OR HDAC7B OR HDAC7 OR KIAA0744.
                                                                                                                                           0.084;
                                                                                                                             Query Match
42.8%; Score 65; DB:
Best Local Similarity 30.3%; Pred. No. 0.08«
Matches 10; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=09UKV0-2; Sequence=VSP_002082;
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SEQUENCE OF 99-650 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=09UKV0-1; Sequence=Displayed;
 send an email to license@isb-sib.ch)
                                    PIR; T31107; T31107.
InterPro; IPR003545; Telomerase_RT.
PRINTS; PR01365; TELOMERASERT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
MEDLINE=99455038; PubMed=10523670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99087487; PubMed=9872452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Interacts with MEF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 3).
                           EMBL; AF060230; AAC39163.1; -.
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                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                       DNA-binding
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HDA9 HUMAN
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/FIId=VSP_002084.
GTGLGEGYNINIAWTGGLD -> RFISLEPHFYLYLSGNCI
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Name 4; Synonyms=HDAC9a;
Isold=Q9UKV0-4; Sequence=VSP 002085, VSP 002086;
SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA
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Shagin D., Usman N., Lukyanov S., Panchin Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1011;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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43ED2785E73CD924 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CO. GO:0005634; C:nucleus; NAS.
GO: GO:0004407; F:histone deacetylase activity; NAS.
GO: GO:0016575; P:histone deacetylation; NAS.
TERPRO IPR00286; His deacetylae.
PF00850; Hist_deacetylse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A (in isoform 4).
/FTId=VSP 002085.
Missing (in isoform 4).
/FTId=VSP_002086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcription regulation; Repressor; Alternative spl
DOMAIN 631 978 HISTONE DEACETYLASE.
ACT SITE 783 783 BY SINGLARITY.
VARSPLIC 487 574 Missing (in isoform 2).
/FTIG-USP_000082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01270; HDÄSUPER.
Hydrolase; Nuclear protein; Chromatin regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L \rightarrow I (I\overline{N} REF. 3)
T -> P (IN REF. 3)
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/FTId=VSP_002083
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      633 AA
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Pred. No. 7
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                                                                                                                                                                                                                                                                                                            EMBL, AY032737; AAK66821.1; -.
EMBL, AY03738; AAK66822.1; -.
EMBL, AB018287; BAA34464.1; -.
EMBL, AF124924; AAF04254.1; -.
Genew; HGNC:14065; HDAC9.
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40.0%;
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                                                                         FAMILY. HD SUBFAMILY 2.
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By Scource From V. Carland J. B. Brashlawich R. Beare D. M., and the control of the body. Carland J. B. Beare D. M., and the control of the body. Carland J. B. Beare D. M., and the control of the body. Carland J. B. Beare D. M., and the control of the body. Carland J. B. Beare D. M., and the control of the body. Carland J. B. Beare D. M., and the control of the body. Carland J. B. Beare D. M., and the control of the body. Carland J. B. Beare D. M., and the control of the contro
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PRINTS; PR00985; TRNASYNTHLEU.

PROSTE; PS00178; AA TRNA LIGASE 1; 1.

Aminoacy1-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Mitochondrion; Transit peptide MITOCHONDRION (BY SIMILARITY).

TRANSIT 1 9 MITOCHONDRION (BY SIMILARITY).

GHAIN 10 894 LEUCYL-TRNA SYNTHETASE.

STTE 56 66 "HTGH" PFGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Herbert C.J., Dujardin G., Labouesse M., Slonimski P.P.; "Divergence of the mitochondrial leucyl tRNA synthetase genes in two closely related yeasts Saccharomyces cerevisiae and Saccharomyces douglasii: a paradigm of incipient evolution."; Mol. Gen. Genet. 213:297-309(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i. CATALYTIC ACTIVITY: ATP + L.leucine + tRNA(Leu) = AMP + diphosphate + L.leucyl-tRNA(Leu).
-i. SUBCELLULAR LOCATION: Mitcohondrial matrix.
-i. SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces douglasii (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=46617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herbert C.J., Labouesse M., Dujardin G., Slonimski P.P.; "The NAM2 proteins from S. cerevisiae and S. douglasii are mitochondrial leucyl-tRNA synthetases, and are involved in mRNA
                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1990 (Rel. 13, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Leucyl-tRNA synthetase, mitochondrial precursor (EC 6.1.1.4)
(Leucine--tRNA ligase) (LeuRS).
                                                                                                                                                                                                         Score 52; DB 1; Length 633;
                                                                                                                                                                                                                                                                   9; Indels
                                                                                   Missing (in isoform 2).
/FTId=VSP 002677.
C89CF833E0251D58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                302 LFIFRKSNFIFDKLHKVGIKTRRQWRRSQFCDIN 335
                                                                                                                                                                                                                                                                                                                           1 LFFYRKS--VWSKLQSIGI--RQHLKRVQLRDVS 30
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8; Mismatches
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                              POTENTIAL.
POTENTIAL
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InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_l
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01-JAN-1990 (Rel. 13, Last seq
                                                                                                                                                    69478 MW;
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Best Local Similarity 38.4.
Best Local 3 Conservative
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EMBO J. 7:473-483(1988).
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136
239
305
124
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114
217
283
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SYLM_SACDO
ID_SYLM_SACDO
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PIR; A64432; A64432.
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                                                                                                                                S-JUL-1998
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16-OCT-2001
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ID YHO7_YEA
AC P38890;
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                                                                                                                                                                                                                   01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-1990 (Rel. 41, Last annotation update)
Nonstructural polyprotein (Contains: Nonstructural protein NSP1;
Nonstructural protein NSP2; Nonstructural protein NSP3; Nonstructural
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88179556; PubMed=2833022;
Faragher S.G., Meek A.D.J., Rice C.M., Dalgarno L.;
"Genome sequences of a mouse-avirulent and a mouse-virulent strain of
Ross River virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                   Ross River virus.";
Virology 163:509-526(1988).
-!- FUNCTION: NSP2 MAY BE INVOLVED IN RNA BINDING DURING REPLICATION.
-!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
-!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE OCCURS.
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
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                                                     Length 894;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NONSTRUCTURAL PROTEIN NSP1.
NONSTRUCTURAL PROTEIN NSP2.
NONSTRUCTURAL PROTEIN NSP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW; E306EBAFDFF02CAB CRC64;
 "KMSKS" REGION.
ATP (BY SIMILARITY).
; AE42C20193DDF107 CRC64;
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                                                     DB 1;
                                                                                                                                                                                              PRT; 2479 AA.
                                                                           7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 18;
                                                                                                                                                                                                                                                                                                 Ross river virus (strain NB5092) (RRV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.2%; Score 52;
55.0%; Pred. No.
                                                     Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro: IPR001788; RNA dep RNApol2.
InterPro: IPR007095; RNA pol DS PS.
InterPro: IPR007094; RNA pol DS PS.
InterPro: IPR007588; V methyltransf.
InterPro: IPR002688; V methyltransf.
                                                                                                                              421 RKSIMGKLHSKGLSKNIIRYRIRD 444
                                                                                                     5 RKSVWSKLQSIGIRQHLKRVQLRD 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00978; RNA dep RNApol2; 1.
Pfam; PF01443; Viral helicase1; 1.
Pfam; PF01660; Vmethyltransf; 1.
SMART; SM00506; Alpp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M20162; AAA96329.1; ALT SEQ.
PIR; A28605; MNWVRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro, IPR002589; Alpp.
InterPro, IPR002620; Peptidase_C9.
                            102193 MW;
                                                   34.2%;
ilarity 41.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2479 AA; 276436
                                                                                                                                                                                              STANDARD;
             649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01661; Alpp; 1
646
649
894 AA;
                                                 Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; C09.001; -.
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Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            Alphavirus.
NCBI TaxID=11031;
                                                                                                                                                                                                                                                                                       protein NSP4].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polyprotein;
CHAIN
                                                                                                                                                                                              POLN RRVN
                            SEQUENCE
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            BINDING
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POLN_RRVN
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Gaps

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7; Indels

7

Conservative

11;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
STRAIN=9633-999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Bordovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical 60.5 kDa protein in SKN7-TWT1 intergenic region.
YHR207C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR003696; Carbtransf.
Pfam; PF02543; CmcH NodU; 1.
Hypothetical protein; Transferase; Complete proteome.
SEQUENCE 609 AA; 71733 MW; C91899CF01CB84EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Euryarchaeota; Methanococci; Methanococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 273:1058-1073(1996).
-!- SIMILARITY: BELONGS TO THE NODU / CMCH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 51.5; DB 1;
Pred. No. 4.8;
                                                                                                                                                                                                                                                                  (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        609 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch)
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                                                        448 FVIPSLWSSSLSIGIRORIK 467
FYRKSVWSKLQSIGIROHLK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.9%;
35.5%;
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                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein MJ1058.
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                                                                                                                                                                                                            STANDARD;
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NAME OF STREET O

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MEDITIES 6041889; PubMed=3903360;
MEDITIES 6041889; PubMed=3903360;
Mehrabian M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,
Kirchgessner T.G., Lin H.-C., Wang X., Ma Y., Mendiaz E., Lusis A.J.;
"Human apolipoprotein B: identification of cDNA clones and
characterization of mRNA.";
Nucleic Acids Res. 13:6937-6953(1985).
                                                                                      MEDLINE=87008488; PubMed=3759943;
Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,
Gotto A.M. Jr., Chan L.;
                                                                                                                                                                                                     complete cDNA and amino acid sequence of human apolipoprotein
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDUINE-87041416; PubMed=3464946;
Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Lackner K.J.,
Lee N., Brewer H.B. Jr.;
"Human liver apolipoprotein B-100 cDNA: complete nucleic acid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-1670 FROM N.A.

BEDLINE=86287313; PubMed=361454;

Protter A.A., Hardman D.A., Sato K.Y., Schilling J.W.,

Yamanaka M., Hort Y.J., Hjerrild K.A., Chen G.C., Kane J.P.;

"Analysis of cNMx clones encoding the entire B-26 region of human apollipoprotein B.";

Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-291 FROM N.A.
MEDLINE-86149325; PubMed-3513177;
Protter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V.,
Protter A.C., Kirsher S.W., McEnroe G., Kane J.P.;
"Isolation of a cDNA clone encoding the amino-terminal region of human apolipoprotein B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1937-2018 AND 3811-4134 FROM N.A.
MEDLINE-86093680; PubMed=3841204;
Carlsson P., Olofsson S.O., Bondjers G., Darnfors C., Wiklund O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 3109-4563 FROM N.A.
MEDLINE=83500528, PubMed=2994225.
Knott T.J. Rall S.C. Jr., Innerarity T.L., Jacobson S.F.,
Urdea M.S., Levy-Wilson B., Powell L.M., Pease R.J., Eddy R.,
Nakai H., Byers M., Priestley L.M., Robertson B., Rall L.B.,
Betsholtz C., Shows T.B., Mahley R.W., Scott J.;
"Human apolipoprotein B: structure of carboxyl-terminal domains,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete sequence and structural analysis of human apolipoprotein B-100: relationship between apoB-100 and apoB-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cladaras C., Hadzopoulou-Cladaras M., Nolte R.T., Atkinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sites of gene expression, and chromosomal localization."; Science 230:37-43(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bjursell G.; "Molecular cloning of human apolipoprotein B cDNA."; Nucleic Acids Res. 13:8813-8826(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 709-906 FROM N.A.
MEDLINE-85270450; PubMed=3860836;
Deeb S.S., Motulaky A.G., Albers J.J.;
"A partial cDNA clone for human apolipoprotein B."
Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human apolipoprotein B.";
Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146(1986)
                                                                                                                                                                                                                                                                             J. Biol. Chem. 261:12918-12921(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 3056-3159 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          derived amino acid sequence.";
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DNA 6:363-372(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1986 (Rel. 03, Created)
01-NOV-1986 (Rel. 03, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipoprotein
                                                                                      MEDLINE=94378003; PubMed=8091229;
MEDLINE=94378003; PubMed=8091229;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Johnston M., Andrews S., Brinkman R., Cooper J., Kirsten J.,
Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEQUENCE FROM N.A. MEDIAGE 3763409; MEDLINE=87016385; PubMed=3763409; MRDLINE=87016385; Wallis S.C., Powell L.M., Pease R.J., Lusis A.J., Lustathar B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.; "Complete cDNA and derived protein sequence of human apolipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88003974; PubMed=3652907;
Ludwig B.H., Blackhart B.D., Pacrotti V.R., Caiati L., Fortier C
Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.;
"DNA sequence of the human apolipoprotein B gene.";
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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48.0%; Pred. No. 5.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 KEQWQKLASISQRE---RIKLRDAS 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 265:2077-2082(1994).
-!- SIMILARITY: Contains 1 SET domain.
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InterPro; IPR001214; SET.
Pfam; PP00856; SET; 2.
SMART; SM00117; SET; 1.
PROSITE; PSS0280; SET; 1.
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Matches 12, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
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Local Similarity 50.0
es 12; Conservative
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057639;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95190020; PubMed=7883971; Pullinger C.R., Hennessy L.K., Chatterton J.E., Liu W., Love J.A., Mendel C.M., Froat P.H., Malloy W.J., Schumaker V.N., Kane J.P.; Heamilial ligand-defective apolipoprotein B. Identification of a new mutation that decreases LDL receptor binding affinity."; J. Clin. Invest. 95:1225-1234(1995).
                                                                                                                                                                                                                                              MEDLINE=87039351; PubMed=3773997;
Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C. Jr.,
Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,
Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W.,
Levy-Wilson B., Scott J.;
"Complete protein sequence and identification of structural domains
of human apolipoprotein B.";
Nature 323:734-738(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T., Tanimura M., Li W.-H., Sparrow D.A., Deloof H., Rosseneu M., Lee F.-S., Gu Z.-W., Gotto A.M. Jr., Chan L.; Sequence, structure, receptor-binding domains and internal repeats of human apolipoprotein B-100."; Nature 323:738-742(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Huang L.-S., Gavish D., Breslow J.L.; "Sequence polymorphism in the human apoB gene at position 8344."; Nucleic Acids Res. 18:5922-5922(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Navajas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P., Cunny G., Cambien F., Roizes G.; "Detection by denaturing gradient gel electrophoresis of a new polymorphism in the apolipoprotein B gene."; Hum. Genet. 86:91-93 (1990).
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MEDLINE-89098975; PubMed=2563166;
Soria L.F., Ludwig E.H., Clarke H.R.G., Vega G.L., Grundy S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20143590; PubMed=10679026; Zhao Y., McCabe J.B., Barthiaume L.G.; Palmitoylation of apolipoprotein B is required for proper intracellular sorting and transport of cholesteroyl esters and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Association between a specific apolipoprotein B mutation and familial defective apolipoprotein B-100."; Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-86242245; PubMed=3087360; , Dashti N., Lee D.M., Mok T.; "Apollopprotein B is a calcium binding protein."; Biochem. Biophye. Res. Commun. 137.49949499(1986).
                     SEQUENCE, AND IDENTIFICATION OF APO-B48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Cell 11:721-734 (2000).
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MEDLINE=91016974; PubMed=2216805;
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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=96337999; PubMed=868087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klank H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
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MEDLINE-97044521; PubMed-8889592; Soliter O., Ricans A.E., Abriter O., Ricand S., Behague I., Souriau C., Evans A.E., Arveiler D., Marques-Vidal P., Luc G., Roizes G., Cambien F.; "Detection of new variants in the apolipoprotein B (Apo B) gene by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . Genet. 102:44-49(1998).
FUNCTION: APOLIPOPROTEIN B IS A MAJOR PROTEIN CONSTITUENT OF CHYLOMICRONS, VLDL AND LDL. IT FUNCTIONS AS A RECOGNITION SIGN FOR THE CELLULAR BINDING AND INTERNALIZATION OF LDL PARTICLES THE APOB/E RECEPTOR.
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                                                                                                                                                                                                                                                                                                                                                        Rabes J.P., Varret M., Saint-Jore B., Erlich D., Jondeau G., Krempf M., Giraudet P., Junien C., Boileau C.; "Familial ligand-defective apolipoprotein B-100: simultaneous detection of the ARG3500-->GLN and ARG3531-->CYS mutations in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leren T.P., Bakken K.S., Hoel V., Hjermann I., Berg K.; "Screening for mutations of the apolipoprotein B gene causing hypocholesterolemia."; Hum. Genet. 102:44-49(1998)
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01-NOV-1997 (Rel. 35, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJ0175.
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50.0%; Pred. No. 60;
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                                                                                                                                                                                                                                                                                 VARIANTS FDB GLN-3527 AND CYS-3558.
MEDLINE-97403938; PubMed-9259199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hum. Mutat. 10:160-163(1997).
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                                                                                                                                                                 SSCP.";
Mutat. 8:282-285(1996)
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SYRBBRRS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Terrahymena thermophila.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
Tetrahymenina; Tetrahymena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7077478;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Telomerase reverse transcriptuse (EC 2.7.7.-) (Telomerase catalytic subbunit) (Telomerase subunit Pl33).
                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                              01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical 108.2 kDa protein in SAP4-OST5 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BMBL; Z72749; CAA66943.1; -.

R PIR; S64249; S64249.

SGD; S0003196; VID30.

R GO; GO:0006008; P:regulation of nitrogen utilization; IMP.

R InterPro; IPR006595; CTLH.

R InterPro; IPR006597; Lish.

R InterPro; IPR006597; SPRY; I.

R SMART; SM00667; Lish; I.

R SMART; SM00667; Lish; I.

R RAART; SM00667; Lish; I.

R RAART; SM00667; Lish; I.

R PROSITE; PSS0897; CTLH; I.

R PROSITE; PSS0897; CTLH; I.
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                                                                                                                                                                                                                                                                                                                               Fartmann B., Kramer B., Kramer W.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILATTY: Contains 1 LisH domain.
-!- SIMILARITY: Contains 1 CTLH domain.
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453 POLY-SER.
108178 MW; 335ADD152949F8C8 CRC64;
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                                                                           958 AA
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nes 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=5911;
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ID TERT TETTH
                                                                           YGX7 YEAST
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YGX7_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Last sequence update)
Telomerase reverse transcriptase (BC 2.7.7.-) (Telomerase catalytic subunit) (Telomerase subunit P123).
Euplotes aediculatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97274210; PubMed=9110970;
Lingner J., Hughes T.R., Shevchenko A., Mann M., Lundblad V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Alveolata; Ciliophora; Spirotrichea; Hypotrichia;
Euplotida; Euplotidae; Euplotes.
NCBI_TaxID=5940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
TELOMERASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1031;
                                                                                                                                                                                              Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Reverse transcriptase motifs in the catalytic subunit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-binding.
SEOUENCE 1031 AA; 122562 MW; 57B87A63A1FED60F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                              Interpro; IPR002848; Translin.
Pfam; PF01997; Translin; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 222 AA; 26425 MW; 9FBBB385C9FFD3D3 CRC64;
                                                                                                                                                                                            Query Match 32.9%; Score 50; DB 1; Best Local Similarity 53.3%; Pred. No. 2.7; Matches 8; Conservative 6; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.9%; Score 50; DB 1; 28.1%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  469 YYYRKNIWDVIMKMSIADLKKETLAEVQEKEV 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Mismatches
send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000477; RVTse.
InterPro; IPR003545; Telomerase_RT.
Pfam; PF00078; rvt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01365; TELOMERASERT
                                                                                                                                                                                                                                                                                                    :|:::|||||||:
203 IQNLKLREHLKRVQI 217
                                      EMBL; U67474; AAB98160.1; -. PIR; H64321; H64321.
                                                                                                                                                                                                                                                                              56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U95964; AAC47515.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Conservative
                                                                                                                                                                                                                                                                         12 LOSIGIROHLKRVQL
                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                               FIGR; MJ0175;
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RESULT 12

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FROM N.A. (ISOFORM 2).
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Nature 408:106-111(2000).
                                                                                                                                                                                       code for large proteins
DNA Res. 5:31-39(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autologous antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=11114197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=11081517;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5,
                                                                                                                                                         ribonucleoprotein complex.",
Proc. Natl. Acad. Sci. U.S.A. 95:8485-8490(1998).
-!- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR
THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT
ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTAGE THAT ADDS
SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE
SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINEm99238449; PubMed=10220385;
Grozinger C.M., Hassig C.A., Schreiber S.L.;
"Three proteins define a class of human histone deacetylases related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01365; TELOMERASERT.
Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
                                                                                                        SEQUENCE FROM N.A.
MEDLINE=98337941; PubMed=9671704;
Collins K., Gandhi L.;
"The reverse transcriptase component of the Tetrahymena telomerase
                                                Bryan T.M., Sperger J.M., Chapman K.B., Cech T.R.; Telomerase reverse transcriptase genes identified in Tetrahymena thermophila and Oxytricha trifallax.". Proc. Natl. Acad. Sci. U.S.A. 95:8479-8484 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
TELOMERASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1117 AA; 133317 MW; E5AF15E86B0F0CD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       roc. Natl. Acad. Sci. U.S.A. 96:4868-4873(1999).
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             090016; 060340; 060528; 0960V4;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Historne deacetylase 5 (HD5) (Antigen NY-CO-9)
HDACS OR KIAA0600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1122 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.6%; Score 48; DB 34.5%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LFFYRKSVW---SKLQSIGI-RQHLKRVQ 25
                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; T14891, T14891.
InterPro, IPR000477; RVTse.
InterPro, IPR003545; Telomerase_RT.
                                   MEDLINE=98337940; PubMed=9671703;
                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF062652; AAC39135.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                            AF061284; AAC39140.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           rvt; 2.
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             FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00078;
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Strausberg R.L., Feingrad E.T., Grouse L.H., Derge J.G.,

Altschul S.F., Zeberg B., Buetow K.H., Schaefer C.F., Bhtr N.K.,

Altschul S.F., Zeberg B., Buetow K.H., Schaefer C.F., Bhtr N.K.,

Hopkins R.F., Jordan H., Morre T., Mars S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Estapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Human and monie chan initial analysis of more than 15,000 full-length
                                 Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T., "Construction of expression-ready cDNA clones for KIAA genes: manual curation of 330 KIAA cDNA clones.";
DNA Res. 9:99-106 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ል
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unidentified human genes. IX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Prediction of the coding sequences of unidentified human genes. IX The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McKinsey T.A., Zhang C.-L., Lu J., Olson E.N.;
"Signal-dependent nuclear export of a histone deacetylase regulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION, PHOSPHORYLATION, AND MUTAGENESIS OF SER-259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=11509672;
McKinsey T.A., Zhang C.-L., Olson E.N.;
Identification of a signal-responsive nuclear export sequence in
class II histone deacetylases.";
Mol. Cell. Biol. 21:6312-6321(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERACTION WITH 14-3-3, AND PHOSPHORYLATION OF SER-249 AND 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEAR EXPORT SIGNAL, AND MUTAGENESIS OF VAL-1086 AND LEU-1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McKinsey T.A., Zhang C.-L., Olson B.N.; "Activation of the myocyte enhancer factor-2 transcription fact calcium/calmodulin-dependent protein kinase-stimulated binding
                                                                                                                                                                                                                                                                                                                                                                                                        Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Colorectal carcinoma;
MEDLINE=98772252; PubMed=961.0721;
Scanlan M.J., Chen Y.-T., Williamson B., Gure A.O., Stockert
Gordan J.D., Tureoto O., Sahin U., Pfreundschub M., Old L.J.;
"Characterization of human colon cancer antigens recognized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 97:14400-14405 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 189-1122 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                               SEQUENCE OF 407-1122 FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SER-279; SER-498; SER-661 AND SER-713.
MEDLINE=22158633; PubMed=12168954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Eye;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
MEDLINE=98290545; PubMed=9628581;
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Hydrolase, Nuclear protein, Chromatin regulator,
Transcription regulation, Repressor, Phosphorylation, Ubl conjugation,
                                                                                                                                                                                                                                                                           GO:0005634; C:nucleus; TAS.
GO:0004407; F:histone deacetylase activity; TAS.
GO:0006342; P:chromatin allending; TAS.
GO:0006355; P:regulation of transcription, DNA-dependent; TAS.
                                                                                                                                                                                                                                                                                    GO:0005737; C:cytoplasm; TAS.
                                                                                                                                                                                                                                                                                                       PRINTS; PR01270; HDASUPER
                                                                                                                                                                                                                                                             HGNC:14068; HDACS
                                                                                                                                                                                                                                                                                                                      Alternative
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HISTONE DEACETYLASE.
NUCLEAR EXPORT.
POLY-GLY.
POLY-GLU.

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                                  Note=No experimental confirmation available, TISSUE SPECIFICITY: Ubiquitous.
DOMAIN: The nuclear export sequence mediates the shuttling between the nucleus and the cytoplasm (By similarity).
PTM: Phosphorylated by CaMK at Ser-259 and Ser-498. The phosphorylation is required for the export to the cytoplasm.
PTM: Ubiquitinated. Polyubiquitination however does not lead
                                                                                                                                                                                                                                                                                         allowing the expression of myoove enhancer factors.
SUBJUNIT: Interacts with HDAC7 and NCOR2 [By similarity). Interacts
SUBJUNIT: Interacts with a 14-3-3 chaperone protein.
SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Shuttles between
the nucleus and the cytoplasm. In muscle cells, it shuttles into
the cytoplasm during myocyte differentiation. The export to
cytoplasm depends on the interaction with a 14-3-3 chaperone
protein and is due to its phosphorylation at Ser-259 and Ser-498
DO CAMK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to its degradation.
SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA
FAMILY: HD SUBFAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ref.5 sequence differs from that shown due to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lsoId=Q9UQL6-2; Sequence=VSP 002081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q9UQL6-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AF132608; AAD29047.1; -.
EMBL, BAD11172; BAA2526.2; ALT INIT.
BEBL; BC011140; AAH13140.1; ALT FERN.
EMBL; AF033691; AAC18040.1; ALT_FRAME.
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Gaps
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0
            Score 48; DB 1; Length 1122;
Pred. No. 32;
                                               7; Indels
                                                 7; Mismatches
                                                                                                                                                                  Search completed: November 12, 2003, 19:48:03 Job time : 7.22642 secs
                                                                                                    :|:||:|| |: :|: |
712 QSIWSRLQETGLLSKCERIRGR 733
                                                                                 6 KSVWSKLQSIGIRQHLKRVQLR 27
              31.6%;
36.4%;
Query Match
Best Local Similarity 36.3
Best Local Similarity
Best Conservative
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. 0

S->A: NO EFFECT.
S->A: REDUCES CAWK-DEPENDENT
PHOSPHORYLATION AND THE SUBSEQUENT
NUCLEAR EXPORT. ABOLISHES NUCLEAR EXPORT
WHEN ASSOCIATED WITH A-259.

279

279

593 E -> D (IN REF. 2).
671 S -> N (IN REF. 5).
684 G -> S (IN REF. 5).
1026 E -> K (IN REF. 5).
1074 E -> G (IN REF. 5).
1093 S -> L (IN REF. 5).
121991. MW; CF4BBBBBBA288FEC CRC64;

671 684 1026 1074

684 1026 1074

1093 À.

S->A: NO EFFECT. S->A: NO EFFECT.

PHOSPHORYTATION AND THE SUBSEQUENT NUCLEAR EXPORT. ABOLISHES NUCLEAR EXPORT WHEN ASSOCIATED WITH A-498.

S->A: REDUCES CAMK-DEPENDENT

V->A: REDUCES CAMK-DEPENDENT NUCLEAR REDUCES CAMK-DEPENDENT NUCLEAR

(in isoform 2). SP 002081.

/FTIG=VSP Missing

EXPORT.

1092 259

259

1086

1086 1092

CAMK)

BY SIMILARITY.
PHOSPHORYLATION (BY CAMK)
PHOSPHORYLATION (BY CAMK)

11104 833 259 498 768

259 498 684

Perfect score:

Title:

Seguence:

OM protein -

Run on:

Scoring table:

Searched:

Minimum DB seq Maximum DB seq

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Database

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Ogeabl chimpanzee
Ogerh5 mus musculu
Ogeq16 mus musculu
Ogeq16 mus musculu
Ogyvd6 anabaena sp
Oss9w3 arabidopsis
Oglow3 treophila
Oglow3 treoph
                                                                                                                                                                                                                                                                                                                                                                                     Q8uj24 agrobacteri
Q8uj24 schizosacch
Q94f92 schizosacch
Q8wui4 homo sapien
Q9uyk9 homo sapien
Q9ugu7 homo sapien
Q9czc9 mus musculu
Q8czc9 ms musculu
O94f41 schizosacch
                                                                                                                                                                                                                                                                                                                                                    Q8j308 pyrococcus
O13295 penicillium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hisatomi H., Nagao K., Kanamaru T., Hirata H., Miyachi K., Hikiji H.;
"Exon 11 deleted variant of human reverse transcripatse.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB086550; BAC11015.1;
InterPro; IPR003545; Telomerase_RT.
PRINTS; PR01365; Telomerase_RT.
PRINTS; PR01365; Telomerase_RT.
SEQUENCE 795 AA; 88965 MW; 6BEAC8A6D1A2E8CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 145; DB 4; Lengtn / ...
Pred. No. 1.9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
ABG-deleted variant of telomerase reverse transcriptase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     795 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              807 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LFFYRKSVWSKLOSIGIRQHLKRVQLRDVS 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                  G9EAB1
G9ERH5
G9EUN6
G8YVD6
G9SGA
G9JGK9
G9JGK9
G9SDQ2
G9S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QBN6C3 PRELIMINARY; PRT;
QBN6C3;
01-OCT-2002 (TrEMBLrel. 22, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                            QBWUI4
Q9NYK9
Q9UFU7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.4%;
93.3%;
   28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
 Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Stomach;
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08NG38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8NG38
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 28NG38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8ng38 homo sapien
Q8ng46 homo sapien
Q8ng46 homo sapien
Q9r0b3 mus musculu
Q9jk99 rattus norv
Q9qxx4 mesocricetu
Q9ds2 xenopus lae
Q818z6 sterkiella
Q8ng79 homo sapien
Q8nug8 paramecium
Q8nug8 paramecium
P90634 leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8tp60 methanosarc
Q8s6n4 oryza sativ
Q28473 macaca fasc
Q13788 homo sapien
                                                                                                                                           (without alignments)
269.937 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                        2003, 19:42:29 ; Search time 28.6792 Seconds
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Q13788
                                                                                                                                                                                                                                                                                                                                                                    830525
                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                 152
1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                            830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                       protein search, using sw model
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QBNGC3
QBNGC3
QBNG46
QBNG9
QBJK39
QBJE32
QB18Z6
QB18Z7
QB18Z7
QBNB79
QBNB79
QBNB79
QBNB79
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Q28473
Q13788
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sp_organelle:*
sp_bhage:*
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sp_plant:*
sp_virus:*
sp_virus:*
sp_virus:*
sp_virus:*
sp_virus:*
sp_virus:*
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sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_bacteriap:*
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length: 2000000000
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Match Length
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1128
11128
11108
11135
768
896
330
                                                                                                                         November 12,
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Gaps

Score

Result Š.

Gaps

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Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                              SEQUENCE FROM N.A.
Drissi R., Cleveland J.L.;
Sequence of a Mus musculus telomerase catalytic subunit intron.";
Subunited (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF090439; AADS4013.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13. Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
10-OCT-2002 (TrEMBLrel. 22, Last annotation update)
10-OCT-2002 (TrEMBLrel. 22, Last annotation update)
10-OCT-2002 (TrEMBLrel. 22, Last Encorate, Encorate, Encorate, Metazoa, Chordate, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         th 89.5%; Score 136; DB 11; Length 575; Similarity 83.3%; Pred. No. 3.2e-12; Similarity 5; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                    89.5%; Score 136; DB 11; Length 52; 83.3%; Pred. No. 2.6e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WONG S., Gao S., Xu X., Yu H.;
"Rat telomerase catalytic subunit, rTERT.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF247818; AF46217.1; -.
InterPro; IPR000477; RVTse.
InterPro; IPR003545; Telomerase_RT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 575 AA; 65672 MW; F80C81BD7F6A91A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                              52 AA; 6479 MW; 41473425E44BDA9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  575 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR01365; TELOMERASERT.
RNA-directed DNA polymerase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Telomerase catalytic subunit (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Mus musculus (Mouse)
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NCBI_TaxID=10036;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                        TISSUE=Stomach cancer;
Hisatomi H., Nagao K., Kanamaru T., Sumida H., Hirata H., Yamamoto M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                             "Both beta and gamma deletion isoform of human telomerase reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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Pred. No. 2.6e-13;
2; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 145; DB 4; Length 807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hisatomi H., Nagao K., Hirata H., Hikiji K., Kanamaru T.; "Exon 11 deleted variant of the human telomerase reverse transcriptase."; Exon 12 deleted variant of the human telomerase reverse submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AB085628; BAC11010.1; -. InterPro; IPR003545; Telomerase_RT. PRINTS; PRELOMERASERT. FRA-directed DNA polymerase. SEQUENCE 1069 AA; 120047 MW; BELE77A653BlC666 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB086379; BAC11014.1; -.
InterPro; IPR003545; Tellomerase_RT.
PRINTS; PR01365; TELOMERASERT.
SEQUENCE 807 AA; 90225 MW; 199664460CE6D763 CRC64;
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Beta and gamma deletion isoform of telomerase reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
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Best Local Similarity 93.3%;
Matches 28; Conservative
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Best Local Similarity
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Q9R0B3;
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EMBL; AK097178; BAC04971.1; -.
InterPro; IPR000286; His_deacetylse
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Best Local Similarity 30.33
Matches 10; Conservative
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Best Local Similarity
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01-MAR-2003
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                                                                                         NON TER
SEQUENCE
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MEDLINE=21240330; PubMed=11342218;
Guo W., Okamoto M., Lee Y.M., Baluda M.A., Park N.H.;
"Enhanced activity of cloned hamster TERT gene promoter in transformed
                                                                                                                                                                                                                                                                                                                               Gaps
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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NCBI_TaxID=200599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.3%; Score 113; DB 13; Length 1191; ilarity 66.7%; Pred. No. 2.3e-08; Conservative 7; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                  Query Match 76.3%; Score 116; DB 11; Length 1128; Best Local Similarity 66.7%; Pred. No. 7.5e-09; Matches 20; Conservative 8; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Telomerase reverse transcriptase of Xenopus laevis.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
BMBL, AF212299, AAG43537.1; -.
InterPro; IPR00477; RVTse.
InterPro; IPR004545; Telomerase_RT.
Pfam; PF00078; rvt; 2.
PRINTS; PR01365; TELOMERASERT.
RNA-directed DNA polymerase; Transferase.
SEQUENCE 1191 AA; 138016 MW; 9BD9D776869AS7D6 CRC64;
                                                                                                                                                                      Pfam; PF00078; rvt; 1.
PRINTS; PR01365; TELOMERASERT.
RNA-directed DNA polymerase; Transferase.
SEQUENCE 1128 AA; 128394 MW; 1D4P81249012174E CRC64;
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Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1191 AA
                                                                                                                                                                                                                                                                                                                                                                                                                  567 LFFYRKSMWRRLQSIGVRHHLERVRLQELS 596
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                                                                                   Biochim. Biophys. Acta 1517:398-409(2001)
BMB1, AR149012; AR17334-1; -.
InterPro; IPR000477; RVTse.
InterPro; IPR001545; Telomerase_RT.
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
Telomerase (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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tes 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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NCBI_TaxID=200599;
                                                                                                                                                                                                        Length 1108;
"The macronuclear telomerase gene in two closely related Stichborichous ciliates.", Submitted (MAX-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AX116502; AAN87867.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Marandi S.S., Prescott D.M.;
"The macronuclear telomerase gene in two closely related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY116501; AAN87866.1;
SEQUENCE 1135 AA, 134341 MW; 3661E5D9300A4942 CRC64;
                                                                                                                                                   1108 AA; 131535 MW; EC8262E01B8E0FAD CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                           Score 65; DB 5;
Pred. No. 0.46;
                                                                                                                                                                                                                                                                                                                                                                 548 IFYYRKNIWNMIMRLSIDDLLKQNLKQVEKKEM 580
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Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P., A fizhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A., Allen N., Maylor J., Stange-Thomann N., DeArellano K., Johnson R., Linton L., McZwan P., McKernan K., Talamas J., Tirrell A., Ye W., A Hedderich R., Ingram-Smirh C., Kuetrner H.C., Krzycki J.A., Guss A.M., A Hedderich R., Ingram-Smirh C., Kuetrner H.C., Krzycki J.A., Ligh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., Frichett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E., A. Metcalf W.W., Birren B.; The genome of Methanosarcina acetivorans reveals extensive metabolic Genome Res. 12:532-544(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 17; Length 378;
                                                                                                                                                       Query Match 34.2%; Score 52; DB 5; Length 330; Best Local Similarity 56.0%; Pred. No. 13; Matches 14; Conservative 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanosarcina acetivorans.
Archaea: Euryarchaeota; Methanococci; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
NCBI_TaxID=2214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein; Complete proteome.
SEQUENCE 378 AA; 42942 MW; 2F628946601E3121 CRC64;
                                                                                               239 239 Q -> *.
330 AA; 38021 MW; A46F0DCB821A554A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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Last sequence update)
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InterPro; IPR001450; 4Fe45 ferredoxin.
InterPro; IPR001395; Aldo/Ket_red.
Pfam; PF00248; aldo_ket_red; I.
Pfam; PF00037; fer4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD000288; Aldo/ket_red; 1.
PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
                                                                                                                                                                                                                                        4 YRKSVWSKLQSIGIRQHLKRVQLRD 28
                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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STRAIN=C2A / ATCC 35395 / DSM 2834;
MEDLINE=21929760; PubMed=11932238;
                SMART, SM00184; RING; 1.
PROSITE, PS00518; ZP RING 1; 1.
PROSTIE; PS50089; ZF RING 2; 1.
Metal-binding; Zinc; Zinc-finger.
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2002 (TrEMBLrel. 22,
Hypothetical protein MA2058.
Pfam; PF00097; zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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es 10; Conser
                                                                                                                    SEQUENCE
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Q8TP60
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AC Q8S6N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A unique pause pattern during telomere addition by the error-prone telomerase from the ciliate Paramecium tetraurelia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
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                                                                            Length 768;
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InterPro; IPR000477; RVTse.
InterPro; IPR003545; Telomerase_RT.
Pfam; PF00078; rvt; 2.
PRINTS; PR01355; TeloMERASERT.
RNA-directed DNA polymerase; Transferase.
SEQUENCE 896 AA; 107237 MW; 697031F9DD61A883 CRC64;
                    Hypothetical protein. SEQUENCE 768 AA; 84836 MW; D47A16B47F4C25E2 CRC64;
                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Last annotation update)
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                                                                              DB 4;
                                                                                                                                                                                                                                                                                                      896 AA.
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                                                                                                                      6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
                                                                              36.2%; Score 55; DB 40.0%; Pred. No. 11;
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                                                                                                                                                             6 KSVWSKLQSIGIRQHLKRVQLRDVS 30
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  Pfam; PF00850; Hist_deacetyl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity 33.33
Matches 10; Conservative
                                                                                                                      Conservative
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                                                          Leishmania donovani.
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RESULT 12

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Indels

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STRAIN-CV. Nipponbare;
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
Overton II L.L., Bera J.J., Tsitrin T., Krol M.L., Jarrahi B.B.,
Jin S.S., Koo H., Zismann V., Haizo J., Blunt S., Vanaken S.S.,
Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
"Oryza sativa chromosome 10 BAC OSJNBa0073L01 genomic sequence.",
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                              Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, Liliopsida; Poales, Poaceae,
Ehrhartoideae, Oryzeee, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca fascicularis (Grab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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Pape M.E., Castle C.K., Murray R.W., Funk G.M., Hunt C.E.,
Marotti K.R., Melchior G.W.;
Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional regulation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 33.6%; Score 51; DB 10; Length 729; Best Local Similarity 40.0%; Pred. No. 41; Matches 10; Conservative 6; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murray R.;
Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; X15737; CAA33755.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUB=Liver;
Marotti K.R.;
Submitted (JUL-1989) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01535; PPR; 9. TIGREAMS; TIGREAMS; TIGREAMS; TIGRO0756; PPR; 8. PROSITE; PS01319; RBFA; 1. Hypochetical protein. SEQUENCE 729 AA; 79961 MW; C9998DA8DB7B5C43 CRC64;
01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical 80.0 kDa protein.
OSJNBA0073L01.16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 RKSVWSKLQSIGIRQHLKRVQLRDV 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last seq 01-DEC-2001 (TrEMBLrel. 19, Last ann Apolipoprotein B (Fragment).
                                                                                                                                                                                                                                                                                                                   Interpro; IPR002885; PPR.
Interpro; IPR000238; Rib_bind_factA.
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                                                                                                          NCBI_TaxID=39947;
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Q28473;
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                             Length 596;
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596 AA; 66757 MW; B13BBA74E25C3120 CRC64;
                              DB 6;
                             Score 50.5; I
Pred. No. 40;
                                                        3; Mismatches
                                                                                                                                                              Search completed: November 12, 2003, 19:50:46 Job time : 29.8459 secs
                                                                                                              521 YGKSLWDFLKLDVTTSIGRRQHLR 544
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hEST2, a human tel
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prognosis; cell proliferation; cancer; ageing; ribonucleoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human telomerase reverse transcriptase antigenic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                  AAY00651
AAY00639
AAY00648
AAW01349
AAY00643
AAY00640
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           AAW97384
AAY00636
AAY25463
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AAY22090
AAY28401
AAY200623
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96US-0724643.
97US-0844419.
97US-081843.
97US-0851843.
97US-081312.
97US-091312.
 97GB-0020890
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06-MAY-1997;
09-MAY-1997;
14-AUG-1997;
14-AUG-1997;
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01-OCT-1996;
18-APR-1997;
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 antigenic.
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 Human telomerase r
Human telomerase r
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       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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139
1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27
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AAW57396
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Gapop 10.0 , Gapext 0.5
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Result

Lingner J;

Harley C,

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telomerase reverse transcriptase (HTRT), from the present invention. The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein preparation of hTRT with a telomerase RNA component; (C) detection of the hTRT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of complex or amplification product with presence of the complex or amplification product with presence of the transcription of a vertebrate cell by increasing the proliferation of a vertebrate cell by increasing the proliferation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polynucleotide encoding hTRT can be used in the manufacture of medicaments for inhibiting the used to treat conditions that are associated with high telomerase contentials.
                                                                                                                                                                                                                                                      variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing
                                                                                                                                                                                                                                                                                                                                                                                present sequence represents an antigenic peptide from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Catalytic telomerase; diagnosis; disease; telomerase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 139; DB 19; 100.0%; Pred. No. 9e-16; Wiemarches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PALLISRLRFIPKPDGLRPIVNMDYVV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 PALLTSRLRFIPKPDGLRPIVNMDYVV
                                                                                                                                               Chapman KB,
Harley CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW97385 standard; Protein; 131 AA.
                                                                                                                                                                                                                                                                                                                                           Example 8; Fig 54; 387pp; English.
97US-0854050.
97US-0911312.
97US-0912951.
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                                                                                                    UNIV TECHNOLOGY CORP
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Best Local Similarity 100.
Matches 27; Conservative
                                                                                                                                               Andrews WH, Cech TR,
Morin GB, Nakamura T,
                                                                                                                                                                                                               WPI; 1998-171633/16.
                                                                                     (GERO-) GERON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JP11046768-A
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    09-MAY-1997;
                       14-AUG-1997;
                                         14-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-FEB-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                          (UXTE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                       The present sequence represents an antigenic peptide from human telomerase reverse transcriptase (hTRT), from the present invention. The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contecting a protein preparation of hTRT with a telomerase RNA component; (C) detection of the hTRT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of hTRT in the sample; and (D) increasing the product with presence of hTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTRT can be used in the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polynucleotide encoding hTRT can be used in the manufacture of medicaments for inhibiting the used to treat conditions that are associated with high telomerase activity and the new holes.
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                                                                                                                                                                     variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and againg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, telomerase reverse transcriptase, hTRT, TRT, diagnosis, prognosis, cell proliferation, cancer, ageing, ribonucleoprotein.
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                                                                 Lingner J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 139; DB 19;
100.0%; Pred. No. 9e-16;
ive 0; Mismatches 0;
                                                                 Harley C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27
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                                                                                                                                                                                                                                                        Example 8; Page 259; 387pp; English.
                                                               Chapman KB,
Harley CB;
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                       (UYTE-) UNIV TECHNOLOGY CORP.
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97US-0844419.
97US-0846017.
97US-0851843.
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Matches 27; Conservative
                                                               Cech TR,
Nakamura T,
                                                                                                                              WPI; 1998-171633/16.
    (GERO-) GERON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 AA;
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25-APR-1997;
06-MAY-1997;
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                                                                 WH.
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                                                                                     Morin GB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                 Andrews
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AAW57396
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DB 19; Length 27;

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invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT cecombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein properation of hTRT with a telomerase RNA component; (C) detection of the hTRT RNA protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplifying the product with presence of hTRT in the sample, and (D) increasing the proliferation of a vertebrate cell by increasing hTRT expression, and (E) the use of an agent that causes an increase in cell expression, and (E) the use of an agent that causes an increase in cell correlation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polynucleotide encoding hTRT can be used in the manufacture of medicaments for inhibiting the used to treat conditions that are associated with high telomerase contaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HTERT). The invention relates to a monoclonal antibody recognising the HTERT. The antibody can be used for the investigation, diagnosis and treatment of telomerase-related diseases, especially diseases in which telomerase expression is up-regulated e.g. cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New monoclonal antibody recognizing human telomerase catalytic subunit (HTERT) useful for treating and diagnosing cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human telomerase reverse transcriptase; hTERT; antibody; diagnosis; telomerase-related disease; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the human telomerase reverse transcriptase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anazawa
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 259;
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                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 139; DB 19;
100.0%; Pred. No. 1.4e-14;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human telomerase reverse transcriptase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 PALLTSRLRFIPKPDGLRPIVNMDYVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
Les 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-591316/50.
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                                                                                                                                                                                                                                                                                                                                                                            259 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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ID AAY4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human telomerase reverse transcriptase protein from cDNA clone 712562.
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                            New catalytic protein of telomerase of a higher animal and a gene coding it - useful for diagnosis of diseases caused by the change in activity of a telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing
                                                                                                                                                                                            The specification describes a human catalytic telomerase protein. The products are useful in drug compositions for the diagnosis of diseases caused by the change in activity of telomerase. The present sequence appears in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
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                                                                                                                                                                                                                                                                                                                                     Length 131;
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                                                                                                                                                                                                                                                                                                                               ; Score 139; DB 20;
; Pred. No. 6.1e-15;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                              1 PALLTSRIRFIPKPDGLRPIVNMDYVV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 14; 18pp; Japanese
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Harley CB;
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97US-0844419.
97US-0846017.
97US-0851843.
97US-0854050.
97US-0911312.
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Best Local Similarity luv..
Best 27; Conservative
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Nakamura T,
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                  WPI; 1999-208111/18
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                                                                                                                                                                                                                                                                                             131 AA;
                                          N-PSDB; AAX15924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV22379
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14-AUG-1997
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                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
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Matches

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RESULT

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This invention describes novel human CRT-1 genes and their encoded proteins containing a reverse transcriptase motif, which act as telomerase inhibitors. The gene, its encoded protein and derived antibodies can be used to provide base sequence information, detect telomerase activity and cancer cells, and to screen telomerase inhibitors. The detection method is simple and effective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel gene, useful in detection of telomerase activity and cancer cells as well as screening telomerase inhibitors for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, telomerase reverse transcriptase, hTRT, TRT, diagnosis, prognosis, cell proliferation, cancer, ageing, ribonucleoprotein.
                                                                                          CRT-1; reverse transcriptase; telomerase; inhibitor; detection; telomerase activity; cancer cell; screening; human.
                                                                                                                                                                                         11..438
/label= CRT-1
/note= "Partial sequence, no stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 438;
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100.0%; Score 139; DB 20;
Best Local Similarity 100.0%; Pred. No. 2.6e-14;
Matches 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 PALLTSRLRFIPKPDGLRPIVNMDYVV 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 35-36; 44pp; Japanese.
                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW47003 standard; Protein; 514 AA
                                                                                                                                                                                                                                                                                                                     99WO-JP00039
                                                                                                                                                                                                                                                                                                                                                   98JP-0139177
                                                                                                                                                                                                                                                                                                                                                                  98JP-0013232
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                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Yoshida K,
                                                               Human CRT-1 protein #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-430393/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  438 AA;
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                                22-SEP-1999
                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                       WO9935261-A1
                                                                                                                                                                                                                                                                                                                     08-JAN-1999;
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 AAY25462;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel human CRT-1 genes and their encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel gene, useful in detection of telomerase activity and cancer cells as well as screening telomerase inhibitors for treatment of
                                                                                                                                                                                                                                                                                     CRT-1; reverse transcriptase; telomerase; inhibitor; detection; telomerase activity; cancer cell; screening; human.
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100.0%; Pred. No. 2.6e-14;
tive 0; Mismatches 0;
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   Pred. No. 1.5e-14;
                  Mismatches
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                                                                   PALLISELRFIPKPDGLRPIVNMDXVV 92
                                                 1 PALLTSRLRFIPKPDGLRPIVNMDYVV
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/label= CRT-1
100.08;
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98JP-0033584
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                  27; Conservative
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                                                                                                                                                                                                                                                       Human CRT-1 protein #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-430393/36.
N-PSDB; AAX88243.
Best Local Similarity
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Best Local
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Protein
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Gaps

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Best Loc Matches

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UX:

/note= "glutathione-S-transferase fragment"

Location/Qualifiers

/note= "hTRT protein fragment"

249..531

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(first entry)

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Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing
                                                                     Human, telomerase reverse transcriptase; hTRT; TRT; diagnosis;
prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
                                            Glutathione-S-transferase and hTRT fusion protein 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 6; Page 225; 387pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                  GERON CORP.
UNIV TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-171633/16.
                                                                                                                        Homo sapiens
                 13-AUG-1998
                                                                                                                                                                                                                                                                                    01-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morin GB,
                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                   (GERO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYTE-)
                                                                                                                                                               Region
                                                                                                                                                                                         Region
    The present sequence represents a fusion protein from an example of the present invention which describes human telomerase reverse transcriptases (hTRT). The present invention also describes the franscriptases (hTRT). The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant preparation of recombinant telomerase by contacting a protein preparation of recombinant telomerase RNA compound; (C) detection preparation of recombinant telomerase RNA component; (C) detection of probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of hTRT in the sample; and (B) increasing the proliferation of a vertebrate cell by increasing hTRT expression; and (E) the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polymucleotide encoding the effect of ageing or cancer. Inhibitors of telomerase activity can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions that are associated with high telomerase activity. A protein preparation of hTRT can also be used in the new
                                                                                                                                                                                                                                                                                                                                                                                       Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 514;
             1..220
/note= "glutathione-S-transferase fragment"
                                                                                                                                                                                                                                                                                                                          Harley C, Lingner J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 139; DB 19; 100.0%; Pred. No. 3.2e-14;
                                      238..514 Thote: "hTRT protein fragment"
 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Page 226; 387pp; English
                                                                                                                                                                                                                                                                                                                       Chapman KB,
Harley CB;
                                                                                                                                                                       96US-0724643.
97US-0844419.
97US-0846017.
                                                                                                                                                                                                                                                                                          UNIV TECHNOLOGY CORP.
                                                                                                                                                                                                              97US-0851843
97US-0854050
                                                                                                                                   97GB-0020890
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Best Local Similarity 100.(
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                 Andrews WH, Cech TR,
Morin GB, Nakamura T,
                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-171633/16.
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                                                                                                                                  01-OCT-1997;
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                                                                                                                                                                                                                                                                                (GERO-)
                                                                                                                                                                                                                                                                                             (UYTE-)
               Region
                                         Region
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Harley C, Lingner J;

Chapman KB, Harley CB;

Cech TR, Nakamura T,

96US-0724643. 97US-0844419. 97US-0846017. 97US-0851843. 97US-0911312. 97US-0912951.

97GB-0020890 97US-0915503

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The present sequence represents a fusion protein from an example of the present invention which describes human telomerase reverse transcriptase (hTRT). The present invention also describes the transcriptase (hTRT). The present invention also describes the chollowing methods: (A) determining whether a test compound is a modulator of hTRT, by determining whether a test compound is a modulator of hTRT, by determining the change in hTRT recombinant preparation of the compound; (B) preparation of trecombinant telomerase RNA component; (C) detection preparation of hTRT with a telomerase RNA component; (C) detection of the hTRT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of probe to the sample and detecting the complex formed or in the sample; or amplification product with presence of hTRT in the sample; and (D) increasing the product with presence of hTRT in the sample; of hTRT expression; and (E) the use of an agent that causes an increasing cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polynucleotide encoding considered to the defect of ageing or cancer. Inhibitors of telomerase activity can be used in the manufacture of medicaments for inhibiting the cueffect of ageing or cancer. Inhibitors of telomerase activity can be used in the manufacture of medicaments for inhibiting consideration of hTRT can also be used in the new and accordated with high telomerase
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100.0%; Pred. No. 3.3e-14;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 27; Conservative
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Gaps

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Indels

0; Mismatches

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RESULT 9 AAW47002 AAW47002;

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564 AA;
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ID AAY0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is a human telomerase reverse transcriptase (hTRT) clone protein from the present invention. The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contecting a protein preparation of recombinant telomerase by contecting a protein of preparation of recombinant telomerase RNA component; (C) detection of the hTRT with a telomerase RNA component; (C) detection of the hTRT with a telomerase RNA component; (C) detection of amplifying the product and correlating the presence of complex or amplification product and correlating the presence of complex or amplification product with presence of HTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increase in cell correlated (B) the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of HTRT and the polynucleotide encoding hTRT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing
                                                                                                                                                                              Human telomerase reverse transcriptase 63 kDa clone 712562 protein.
                                                                                                                                                                                                         Human, telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
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Harley CB;
                             314 PALLTSRLRFIPKPDGLRPIVNMDYVV 340
             1 PALLISRLRFIPKPDGLRPIVNMDYVV 27
                                                                                                                                                                                                                                                                                                               /label= encoded by ARG
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                                                                                                      AAW56109 standard; Protein; 564 AA.
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9703-0844419.
9703-0846017.
9703-0851843.
9703-0913312.
9703-0913312.
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Morin GB, Nakamura T,
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01-OCT-1996;
18-APR-1997;
25-APR-1997;
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14-AUG-1997;
14-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New catalytic protein of telomerase of a higher animal and a gene coding it - useful for diagnosis of diseases caused by the change in activity of a telomerase
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
used to treat conditions that are associated with high telomerase activity. A protein preparation of hTRT can also be used in the new methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a catalytic telomerase protein. The products are useful in drug compositions for the diagnosis of diseases caused by the change in activity of telomerase.
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                                                                                                                                                       Length 564;
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                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-terminal truncated telomerase protein sequence.
                                                                                                                                                    100.0%; Score 139; DB 19;
100.0%; Pred. No. 3.5e-14;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 PALLISRLRFIPKPDGLRPIVNMDYVV 27
                                                                                                                                                                                                                                                                                                 66 PALLTSRLRFIPKPDGLRPIVNMDYVV 92
                                                                                                                                                                                                                                                          1 PALLISRLRFIPKPDGLRPIVNMDYVV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 11-14; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY00636 standard; Protein; 617 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW97384 standard; Protein; 591 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A catalytic telomerase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MITU ) MITSUBISHI CHEM CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-MAY-1999 (first entry)
                                                                                                                                                                                                      27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-208111/18.
N-PSDB; AAX15923.
                                                                                                                                                         Query Match
Best Local Similarity
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW46997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                 Protein
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                                        Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW46997
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                                                                                                                                                                                                                                                                                                                                                                                  This sequence is a truncated human telomerase of the invention. Primers that amplify the telomerase coding sequence can be used in a method for diagnosing cancer in a patient. The telomerase can be used for detection, diagnosis and drug screening. Inhibitors of telomerase activity can be used to treat cancers such as melanomas, other skin cancers, neuroblastomas, breast carcinomas, cleukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin growths. Enhancers of telomerase may be used to stimulate stem cells proliferation and differentiation (expansion of haematopoietic stem cells could be administered in the bone marrow transplant context). As well, many tissues have stem cells. Proliferation of these cells may be useful in wound healing, hair growth, treatment of disease such as wilm's tumour, organ regeneration or differentiation after injury or diseases, nerve cell or brain cell growth following injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia; neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma; smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour; stem cell differentiation; organ regeneration; organ differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                  New isolated vertebrate telomerase genes - used to develop products for treating cancers or for organ regeneration, nerve cell or brain cell growth following injury or bone marrow transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRT-1; reverse transcriptase, telomerase, inhibitor, detection, telomerase activity, cancer cell; screening, human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 PALLISRLRFIPKPDGLRPIVNMDYVV 27
                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Fig 11b-c; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY25463 standard; Protein; 622 AA.
                                                                                                                                                               97US-0058287.
97US-0051410.
97US-0053018.
97US-0053329.
97US-0054642.
                                                                                                                                                                                                                                   (CAMB-) CAMBIA BIOSYSTEMS LLC
                                                                                                                                           98WO-US13835.
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                                                                                                                                                                                                                                                          Kilian A;
                                                                                                                                                                                                                                                                                WPI; 1999-106060/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        617 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                shown in AAY00653
                                                                                                                                                                                                                                                                                            N-PSDB; AAX18264.
                                                            sapiens
                                                                                           WO9901560-A1
                                                                                                                                          01-JUL-1998;
                                                                                                                                                                                                            04-AUG-1997;
                                                                                                                                                                 39-SEP-1997;
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                                                                                                                   14-JAN-1999
                                                                                                                                                                                                                                                         Bowtell D,
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                                                                                                                                                                                                   21-JUL-1997
                                                                       Synthetic.
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                                                           Ношо
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This invention describes novel human CRT-1 genes and their encoded proteins containing a reverse transcriptase motif, which act as telomerase inhibitors. The gene, its encoded protein and derived antibodies can be used to provide base sequence information, detect telomerase activity and cancer cells, and to screen telomerase inhibitors. The detection method is simple and effective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel gene, useful in detection of telomerase activity and cancer cells as well as screening telomerase inhibitors for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
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                       1..622
/label= CRT-1
/note= "Partial sequence, no stop codon given"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 622;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human telomerase reverse transcriptase Delta182 variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 139; DB 20;
100.0%; Pred. No. 4e-14;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 37-39; 44pp; Japanese.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW46997 standard; Protein; 807 AA.
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Matches 27; Conservative 0
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98JP-0013232.
98JP-0033584.
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96US-0724643.
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                                                                                                                                                                                                                                                                                                                                                                             (CHUS ) CHUGAI SEIYAKU KK.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Yoshida K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-430393/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           622 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAX88251
                                                                                                                                                                                                                            08-JAN-1999;
                                                                                                                                                                                                                                                                           06-MAY-1998;
08-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                               Tsuchiya M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                        W09935261-A1
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This sequence is a truncated human telomerase of the invention. Primers that amplify the telomerase coding sequence can be used in a method for diagnosing cancer in a patient. The telomerase can be used for detection, diagnosis and drug screening. Inhibitors of telomerase activity can be used to treat cancers such as melanomas, other skin cancers, neuroblastomas, breast carcinomas, colon carcinomas, leukaemias, lymphomas, osteosatroomas or smooth muscle cell hyperplasias or skin growths. Enhancers of telomerase may be used to stimulate stem cell proliferation and differentiation (expansion of haematopoietic stem cells could be administered in the bone marrow transplant context). As well, many tissues have stem cells. Proliferation of these cells may be useful in wound healing, hair growth, treatment of disease such as wilm's tumour, organ regeneration or differentiation after injury or diseases, nerve cell or brain cell growth following injury.
                                                                                                                                                                                                                                                                                                                                                  New isolated vertebrate telomerase genes - used to develop products for treating cancers or for organ regeneration, nerve cell or brain cell growth following injury or bone marrow transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Fig 11d-e; 134pp; English.
                                                                                                                                                                                                                                                         Bowtell D, Kilian A;
                                                                                                                                                                                                                                                                                               WPI; 1999-106060/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                               N-PSDB; AAX18265
                                                        01-JUL-1998;
                                                                                                                                                                            04-AUG-1997;
                                                                                                                                   21-JUL-1997;
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                  14-JAN-1999
                                                                                               09-SEP-1997
                                                                                                                   01-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
  The present sequence represents a human telomerase reverse transcriptase (hTRT) variant from the present invention. The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or preparation of recombinant telomerase By contacting a protein preparation of recombinant telomerase By contacting a protein preparation of frecomplant telomerase By contacting a protein of the hTRT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of hTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTRT expression; and (E) the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibite ageing. A protein preparation of hTRT and the polymoclectide encoding hTRT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used in that are associated with high telomerase.
                                                                                                                                                                                                                                                                                                               Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activity. A protein preparation of hTRT can also be used in the
                                                                                                                                                                                                Lingner J;
                                                                                                                                                                                                Harley C,
                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 20; 387pp; English
                                                                                                                                                                                                Chapman KB,
Harley CB;
                970S-0846017.
970S-0851843.
970S-0854050.
970S-0911312.
970S-0912951.
                                                                                                                                                       (UYTE-) UNIV TECHNOLOGY CORP
  97US-0844419
                                                                                                                                                                            Cech TR, C
                                                                                                                                                                                                Andrews WH, Cech TR
Morin GB, Nakamura
                                                                                                                                                                                                                                                         WPI; 1998-171633/16.
N-PSDB; AAV22382.
                                                                                                                                         CORP
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                                                                                                                                       (GERO-) GERON
                                                                            14-AUG-1997;
14-AUG-1997;
                                                                                                                                                                                              WH,
18-APR-1997
                                          06-MAY-1997
                                                            09-MAY-1997
                      25-APR-1997
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(CAMB-) CAMBIA BIOSYSTEMS LLC

97US-0058287. 97US-0051410. 97US-0053018. 97US-0053329.

97US-0054642

98WO-US13835

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100.0%; Score 139; DB 20; I Similarity 100.0%; Pred. No. 5.5e-14; 27; Conservative 0; Mismatcher
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                                                         100.0%; Score 139; DB 19;
100.0%; Pred. No. 5.5e-14;
ive 0; Mismatches 0;
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                                                                                 Conservative
                                                                      Similarity
                                                              Ma.
Local Sir.
27;
                                                           Query Match
                                                                                  Matches
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neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma; smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour; stem cell differentiation; organ regeneration; organ differentiation. Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;

Homo sapiens WO9901560-A1

Synthetic.

N-terminal truncated telomerase protein sequence.

26-JUL-1999 (first entry)

AAY00637;

AAY00637 standard, Protein, 807 AA

RESULT 15 AAY00637

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614 PALLISRLRFIPKPDGLRPIVNMDYVV 640
                                                                                                                                  Search completed: November 12, 2003, 19:47:14
1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27
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Gaps

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Length 807; Indels

807 AA;

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California
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RESULT 1
US-08-851-843A-117
                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                        November 12, 2003, 19:43:50 ; Search time 12.566 Seconds (without alignments) 90.911 Million cell updates/sec
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Sequence 167, 1
Sequence 287, 1
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Sequence 167,
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      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-974-549A-237
US-08-918-91-117
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US-08-912-951-116
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US-08-912-951-10
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US-08-851-843A-101
US-08-974-549A-267
US-08-854-050-101
US-09-430-322-101
US-08-974-549A-5
                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                            1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27
                                                                                                                                                       328717 seqs, 42310858 residues
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Maximum Match 100%
Listing first 45 summaries
                                       OM protein - protein search, using sw model
                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                        Patents AA:*
                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                          US-08-854-050-117
139
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Match Length
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                                                                                                    Perfect score:
                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                       Searched:
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No.
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29 119 100.0 807 4 US.08-18-51-55. Sequence 5.7, Appl. 20 119 100.0 1000 1 US.08-18-61-81-217. Sequence 5.7, Appl. 20 119 100.0 1000 1 US.08-18-61-81-217. Sequence 5.7, Appl. 20 119 100.0 1000 1 US.08-18-61-61-217. Sequence 5.7, Appl. 20 119 100.0 1000 1 US.08-18-61-217. Sequence 5.7, Appl. 20 119 100.0 1100 1 US.08-18-61-217. Sequence 5.7, Appl. 20 119 100.0 1100 1 US.08-18-61-217. Sequence 5.7, Appl. 20 119 100.0 1100 1 US.08-18-61-217. Sequence 5.7, Appl. 20 119 100.0 1101 2 US.08-18-61-225. Sequence 5.7, Appl. 20 119 100.0 1101 2 US.08-18-61-225. Sequence 5.7, Appl. 20 119 100.0 1101 2 US.08-18-61-225. Sequence 5.7, Appl. 20 119 100.0 1101 2 US.08-18-61-225. Sequence 5.7, Appl. 20 119 100.0 1101 2 US.08-18-61-225. Sequence 5.7, Appl. 20 119 100.0 1101 2 US.08-18-61-225. Sequence 5.7, Appl. 20 119 100.0 1101 2 US.08-18-61-225. Sequence 5.7, Appl. 20 119 100.0 1101 2 US.08-18-18-18-2. Sequence 5.7, Appl. 20 119 100.0 1101 2 US.08-18-18-18-2. Sequence 5.7, Appl. 20 119 100.0 1101 2 US.08-18-18-18-2. Sequence 5.7, Appl. 20 119 100.0 1101 2 US.08-18-18-18-2. Sequence 5.7, Appl. 20 119 100.0 1101 2 US.08-18-28-61 3 Sequence 5.7, Appl. 20 119 100.0 1101 2 US.08-19-2-51-325 Sequence 5.7, Appl. 20 119 100.0 1101 2 US.08-19-2-51-325 Sequence 5.7, Appl. 20 119 100.0 1101 2 US.08-19-2-51-325 Sequence 5.7, Appl. 20 110 110 110 110 2 US.08-19-2-51-325 Sequence 5.7, Appl. 20 1
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01-OCT-1997
                                                                                                                                                                                                                                                    LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS:
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CITY: San Francisco
STATE: California
COUNTRY: United State
                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                   US-08-974-549A-237
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Best Local Similarity 100.0%; Pred. No. 3.16-15;
Matches 27; Conservative 0; Mismatches 0. Trann
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cech, Thomas R.
APPLICANT: Cech, Thomas R.
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/974,549A FILING DATE: 19-NOV-1997 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911 111
PLING DATE:
                                                                                                                                                                                                                                    1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APF-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APF-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
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PRIOR APPLICATION DATA:
APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
                  : 27 amino acids amino acid
SEQUENCE CHARACTERISTICS:
                                              TYPANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-851-843A-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                  LENGTH:
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,117
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 139; DB 3;
Best Local Similarity 100.0%; Pred. No. 3.1e-15;
Matches 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 117, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Coch, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Andrews, William H.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: Townsend and Townsend and Crew LLP
Two Embarcadero Center, 8th Floor
                                                                                              NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/STOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELECPHONE: (415) 576-0200
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY AGENT INFORMATION:
NAME: Apple, Randolph Ted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
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. United States of America
                                                                                                                                                                                INFORMATION: (415) 576-0200
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 237:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Linguer, Joachim
APPLICANT: Linguer, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Originan, Karen B.
APPLICANT: Morih, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: THERAPEUTIC METHODS
TITLE OF INVENTION: THERAPEUTIC METHODS
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                                                                                                                                                                                                                                                                     Length 27;
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ZIEP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951

**TITING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 139; DB 4;
Best Local Similarity 100.0%; Pred. No. 3.1e-15;
Matches 27; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Two Embarcadero Center, 8th Floor
                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 117:
                                                                                                                                                                                                                                                                                                                                                            1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
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APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
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United States of America
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FILING DATE: 25-APR-1997
    (415) 576-0200
15) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 116, Application US/08912951
Patent No. 6475789
                                                                                                                  TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
                         TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO: 117:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 06
CLASSIFICATION:
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                                                                                                                                                                                                                            US-09-430-323-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Ca
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COMPUTER: IDAPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                                                                                                                                                      Length 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 139; DB 3; 100.0%; Pred. No. 3.1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                             NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFENCE/COCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 mmino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 117, Application US/09430323 Patent No. 6309867 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
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FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                 TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                        ; MULBCULE 111.
US-08-854-050-117
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GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

APPLICANT: Lingman, Karen B.

APPLICANT: Morin, Greeg B.

APPLICANT: Andrews, William H.

TITLE OF INVENTION:

APPLICANT: Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 30
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telomerase core protein 1 (TCP1)"
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CONTRY: USA

CONTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYEE Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: ISM P
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 139; DB 3;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
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CLASSIPICATION: 536
PRIOR APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
FRIOR APPLICATION DATA: APPLICATION DATA: REPLICATION DATA: US 08/844,419
FILING DATE: 18-APR-1997
FRID APPLICATION DATA: US 08/846,017
APPLICATION NUMBER: US 08/846,017
FRILNG DATE: 25-APR-1997
FRILNG DATE: O6-MAY-1997
FRILNG DATE: 06-MAY-1997
FRILNG DATE: 09-MAY-1997
FRILNG DATE: 09-MAY-1997
FRILNG DATE: 09-MAY-1997
FRILNG DATE: US 08/851,843
FRILNG DATE: US 08/851,843
FRILNG DATE: US 08/851,843
FRILNG DATE: US 08/851,312
FRILNG DATE: US 08/851,312
FRILNG DATE: US 08/851,312
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                                                              LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLLGY: linear
MOLECULE TYPE: peptide
INFORMATION FOR SEQ ID NO:
                               SEQUENCE CHARACTERISTICS LENGTH: 30 amino acid
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                               ; NAME/KEY: Peptide
; LOCATION: 1.30
; OTHER INFORMATION: /
US-08-851-843A-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           San Francisco
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US-08-974-549A-287
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                                                                                                                                                                                                                                   FEATURE:
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ZIP: 94111
COMPUTER SEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A

TILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Harleý, Caľvín
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
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NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                        REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMOUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27
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Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen
APPLICANT: Chapman, Karen
APPLICANT: Morin, Gregg B.
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION:
   Randolph T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.(
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-851-843A-167
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "motif 0 peptide from human
telomerase core protein 1 (TCP1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend and Crew STREET: Two Embarcadero Center, 8th Floor CITY: San Prancisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 139; DB 3; Best Local Similarity 100.0%; Pred. No. 3.5e-15; Matches 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: «Unknown»
CLASSIFICATION: 520

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: APPLICATION: 36
ATTORNEY/AGENT INFORMATION:
NAME: APPLICATION 196
TELECOMMUNICATION: 186,429
REFERENCE/DOCKET NUMBER: 36,429
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27
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Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Ingner, Joachim
NAKamura, Toru
Chapman, Karen B.
Mariey, Calyin
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1.30
CTHER INFORMATION:
CTHER INFORMATION:
US-08-854-050-167
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US-09-430-323-167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "motif 0 peptide from human
telomerase core protein 1 (TCP1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09 MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Greeg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                           PRIOR APPLICATION DATE:

PRIOR DATE: 14-AUG-1997
PRIOR DATE: 14-AUG-1997
PRIOR DATE: 10-AUG-1997
PRIOR APPLICATION DATE:

APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATE: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REJERENCE/DOCKET NUMBER: 36,429
REJERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0300
INFORMATION POR SEQ ID NO: 287:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 PALLTSRLRFIPKPDGLRPIVNMDYVV 29
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APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 167, Application US/08B54050 Patent No. 6261836 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 30 amino acids
               PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Peptide
LOCATION: 1.30
OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-974-549A-287
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PRIOR APPLICATION DATE:

PRIOR APPLICATION UNIMBER: US 08/846,017
PRIOR APPLICATION NUMBER: US 08/851,843
PRIOR APPLICATION NATA:

APPLICATION NUMBER: US 08/854,050
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-CCT-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-CCT-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-CCT-1997
ATTORNEY/AGENT INFORMATION:

REGESTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01.0CT-1997
ATTORNEY/AGENT INFORMATION:

TELEPHONE: (415) 576-0300
INFORMATION POR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
             FILING DATE: 01-OCT-1996
PRIOR APPLICATION UNDATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 31, Application US/08912951; Patent No. 6475789; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1.54
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Peptide LOCATION: 1..54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-974-549A-31
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1..30
OTHER INFORMATION: /note= "motif 0 peptide from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 139; DB 4; Length 30; Best Local Similarity 100.0%; Pred. No. 3.5e-15; Matches 27; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Greeg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 9411-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEUTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                     NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                         FILING DATE: 09-WAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-WAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
                           APPLICATION NUMBER: US 08/854,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     telomerase core protein 1 (TCP1)
SEQUENCE DESCRIPTION: SEQ ID NO: 167:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 PALLTSRLRFIPKPDGLRPIVNMDYVV 29
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APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31, Application US/08974549A
Patent No. 6166178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cech, Thomas R.
Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Cech, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-430-323-167
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HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
                                                                                                                  Gaps
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                                                                       Length 54;
                                                                                                                Indels
/note= "motif 1 and 2 peptide from human TRT"
                                                                           100.0%; Score 139; DB 3; 100.0%; Pred. No. 6.7e-15;
                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THERAPEUTIC METHODS
                                                                                                                                                    1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27
                                                                                                                                                                              10 PALLISELRFIPKPDGLRPIVNMDYVV 36
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/44,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
APPLICATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPAX: (415) 576-0200
INPORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TTENERAMION OC SCI
                            APPLICANT: Chap...
APPLICANT: Morin, Gregg ...
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
ITLE OP INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
"TPEET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1.129
; OTHER INFORMATION: /note= "TRT motifs from human"
US-08-851-843A-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 139; DB 3;
100.0%; Pred. No. 1.8e-14;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 PALLTSRLRFIPKPDGLRPIVNMDYVV 99
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US-08-974-549A-13
IS-08-974-549A-13
Sequence 13, Application US/08974549A
FRACEN NO. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
                                                                                                                                                                                                                                                                                                                           COUNTRY: United States of America ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: 11
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; OTHER INFORMATION: /note= "motif 1 and 2 peptide from ... OTHER INFORMATION: human TRT"
US-08-912-951-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                   COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FLING DATE: 14-ANG-1997
CLASSIFICATION NUMBER: US 08/854,050
FLING DATE: 09-MAY-1997
CLASSIFICATION NUMBER: US 08/854,050
FLING DATE: 09-MAY-1997
CLASSIFICATION NUMBER: US 08/851,843
FLING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/846,017
FLING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/846,017
FLING DATE: 15-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: US 08/724,643
FILING DATE: US 08/724,643
FILING APPLICATION NUMBER: US 08/724,643
FILING DATE: US 08/724,643
FILING DATE: US 08/724,643
                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 139; DB 4;
Best Local Similarity 100.0%; Pred. No. 6.7e-15;
Matches 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTATION NUMBER: 36,425.
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-020
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 PALLTSRLRFIPKPDGLRPIVNMDYVV 36
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                                                                                                                                                  United States of America
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US-08-851-843A-67
; Sequence 67, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 54 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Peptide
                                                                                                                                               COUNTRY: U
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APPLICANT: MOTIN, Gargia B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
CONTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Compatible
OPERATING SYSTEM: PC COMPATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
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LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
ATORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
RECCOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATION PROPER: US 08/844,419
FILING DATE: 18-APR-1997
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
Chapman, Karen B.
Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
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100.0%; Score 139; DB 3; Length 129;

Query Match

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Gaps
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                             Indels
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CUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION SAS
PRIOR APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION SAS
PRIOR APPLICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: 36,429
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: 36,429
REPRENCE/DOCKET NUMBER: 36,429
RELEBRAX: (415) 576-0300
INDOMMATION FOR SEO ID NO: 67: SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TTELEPAX: amono acids
TTELEPAX: amono acids
TTELEPAX: amonomy acids
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LOCATION: 1..129

COTHER INFORMATION: /note= "TRT motifs from human"

US-08-854-050-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSEE: Townsend and Townsend and Crew LLP
I: Two Embarcadero Center, 8th Floor
San Francisco
Best Local Similarity 100.0%; Pred. No. 1.8e-14;
Matches 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingmer, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
                                                                                 1 PALLISRLRFIPKPDGLRPIVNMDYVV 27
                                                                                                              73 PALLTSRLRFIPKPDGLRPIVNMDYVV 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        California
: United States of America
                                                                                                                                                                                                                                                                            Sequence 67, Application US/08854050
Patent No. 6261836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend &
STREET: Two Embarcade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
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US-08-854-050-67
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Query Match
100.0%; Score 139; DB 3; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.8e-14;
Matches 27; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NDATA: PS99

FLING DATE: 29-Oct-1999

CLASSIFICATION NUMBER: US 08/854,050

PRIOR APPLICATION NUMBER: US 08/854,843

PLING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

RILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

ATTORNEY AGENT INFORMATION: MANANAMENT OF TABLES OF TABL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1.129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chaman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: California
COUNTRY: United States of America
                                                                                                                                                                         1 PALLISRLRFIPKPDGLRPIVNMDYVV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 67, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-09-430-323-67
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100.0%; Score 139; DB 4; Length 129;

Query Match

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Sequence:

Run on:

Searched:

Database

Result No.

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Appl
Appl
Appl
Appli
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5, Appli
5, Appli
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Sequence 217, App
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chaman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020164786Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend and Crew STREET: Two Embarcadero Center, 8th Floor
                    US-09-766-253-67
US-09-438-486-67
US-10-054-295-67
US-10-054-611-67
US-10-044-692-13
US-10-044-692-13
US-10-044-539-13
US-10-284-778-10
US-10-294-778-10
US-10-294-778-10
US-10-294-778-10
US-10-044-539-318
US-10-044-539-318
US-10-044-539-317
US-10-044-539-317
US-10-044-539-317
US-10-044-539-317
US-10-044-539-317
US-10-044-539-317
US-10-044-539-317
US-10-053-758-101
US-10-053-758-101
US-10-054-295-101
US-10-054-295-101
US-10-054-295-101
US-10-054-295-101
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US-09-438-486-217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/654,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                              US-10-044-539-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 117, Application US/09843676
Patent No. US20020164786A1
GENERAL INFORMATION:
100.0
100.0
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Sequence 116, App
Sequence 116, App-
Sequence 167, App
Sequence 167, App
Sequence 167, App
                                                                              ; Search time 21.566 Seconds
(without alignments)
215.025 Million cell updates/sec
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Sequence 117, P
Sequence 117, P
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Sequence 117, 2
Sequence 117, 1
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Sequence
Sequence
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1: /cgn2_6/ptodata/1/pubpaa/DCT_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/DCT_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-766-253-117
US-10-053-758-117
US-10-054-295-117
US-10-054-295-117
US-10-044-692-116
US-10-044-539-116
US-09-766-253-167
US-09-766-253-167
US-10-053-758-167
US-10-054-61167
US-10-054-61167
US-10-054-61167
US-10-054-61167
US-10-054-61167
US-10-054-61167
                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                      1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27
                                                                                                                                                                                                                 644079 segs, 171749292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                2003, 19:47:20
                                                      OM protein - protein search, using sw model
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                                                                                                                                                                                       Gapop 10.0 , Gapext 0.5
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Maximum Match 1008
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Maximum DB seq length: 200000000
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                                                                               November 12,
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Match Length
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98::
110::
111::
114::
116::
118::
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Gaps

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Length 27;
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APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US20030009019Alel Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
                                                                                                                                                                                                         Query Match 100.0%; Score 139; DB 10; Best Local Similarity 100.0%; Pred. No. 2.7e-14; Matches 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
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REFERENCE/DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION INFORMATION:
TELECHAND.
                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 117:
                                                                                                                                                                                                                                                                                                                                                               1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27
                                                                                                                                                                                                                                                                                                                                                                                                                          1 PALLTSKLKFIPKPDGLRPIVNMDYVV 27
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PELLING DATE: 12-NOV-1999
CLASSIFICATION 1536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION S36
PRIOR APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAMME: APPDIC, NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States of America ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 117, Application US/09438486
; Publication No. US20030009019A1
STRANDEDNESS: <Unknown>
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TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                          US-09-766-253-117
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-30-2001
CLASSIFICATION NUMBER: 08/846,017
APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020187471A1e1 Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California
                                                MAME: ADDIG TO MANDER TO MANDE M
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ 1D NO: 117:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 139; DB 10; Best Local Similarity 100.0%; Pred. No. 2.7e-14; Matches 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States of America ZIP: 94111
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FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 27 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                     ATTORNEY/AGENT INFORMATION
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Gaps
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          Indels
                                                                                                                                                                                                                                                                                                                                                                       Andrews, William H.
TITLE OF INVENTION: No. US20030044953A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 015389-002930US
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100.0%; Pred. No. 2.7e-14;
ive 0; Mismatches 0;
        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: «Unknown»
PELLIANION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 117:
US-10-054-295-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
                                              1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27
                                                                   1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PALLTSRLRFIPKPDGLRPIVNMDYVV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,429
                                                                                                                                                                                     Sequence 117, Application US/10054295
Publication No. US20030044953A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (415) 576-0200
(115) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                                                              Chapman, Karen B.
Morin, Gregg B.
                                                                                                                                                                                                                                                 Cech, Thomas R.
Lingner, Joachim
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0
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LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEC ID NO: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 27; Conservative
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      27; Conservative
                                                                                                                                                                                                                                                                                             Nakamura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415)
                                                                                                                                               RESULT 5
US-10-054-295-117
      Matches
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                                                                                Length 27;
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                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Andrews, William H.
TITLE OF INVENTION: No. US20030032075A1el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                  ; DB 11;
2.7e-14;
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                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
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FILING DATE: 06-MAY-1997
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FILING DATE: 18-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/724,643
                                                                                100.0%; Score 139; 100.0%; Pred. No. 2
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 117:
US-10-053-758-117
                                                                                                                                                              1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27
                                                                                                                                                                                        Sequence 117, Application US/10053758
Publication No. US20030032075A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 576-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (415) 576-0300
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100.0%;
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                            Query Match
Best Local Similarity 100.0
Matches 27; Conservative
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                     ; MOLECULE TYPE: peptide US-09-438-486-117
TOPOLOGY: linear
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Best Local Similarity
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US-10-053-758-117
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Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
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                                                                                                                                                                                                                                                                                     ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692
                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California COUNTRY: United States of America
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100.0%; Pred. No. 2.7e-14;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: CURRIONNA APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 116:
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APPLICATION NUMBER: 08/912,951
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-044-539-116; Sequence 116, Application US/10044539; Publication No. US20030100093A1; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (415) 576-0200
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Harley, Calvin
Andrews, William H
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Chapman, Karen B
Morin, Gregg B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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                                                                                                                                                                                                                                        Andrews, William H.
TITLE OF INVENTION: No. US20030059787A1el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC comparible
COMPUTER: TEM FC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050

FILING DATE: «UNKNOWN:

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-007-1996
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; SEQUENCE DESCRIPTION: SEQ ID NO: 117:
US-10-054-611-117
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                    Sequence 117, Application US/10054611 Publication No. US20030059787A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 27 amino acids
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                                                                                            APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111
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US-10-044-692-116
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SEQUENCE DESCRIPTION: /note= "motif 0 peptide from human telomerase core protein 1 (TCP1)" SEQUENCE DESCRIPTION: SEQ ID NO: 167:
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Andrews, William H.
TITLE OF INVENTION: No. US20020187471Alel Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSE: Two meend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30
         ADDRESSEE: Townsend and Townsend and Crew LLP
                           STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
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                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/843,676
FLING DATE: 26-Apr-2001
CLASSIFICATION: 346
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
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100.0%; Score 139; U
Best Local Similarity 100.0%; Pred. No. 3.1
Matches 27; Conservative 0; Mismatches
                                                                                              COUNTRY: United States of America ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 PALLTSRLRFIPKPDGLRPIVNMDYVV 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (415) 576-0200
(15) 576-0300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakamura, Toru
Chapman, Karen B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cech, Thomas R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 167
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415)
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US-09-766-253-167
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TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020164786Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                  COMPUTER FAIABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
ODRUTER: IBM FO Compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,539
FLIING DATE: 11-Jan-2002
CLASSIFICATION: 435
                                                                          STREET: Two Embarcadero Center, 8th Floor CITY: Oct. Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 139; DB 15; Best Local Similarity 100.0%; Pred. No. 2.7e-14; Matches 27; Conservative 0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/85,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                    STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-10-044-539-116
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Patent No. US20020164786A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 576-0200
                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (415) 576-0300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 27 amino acids
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                                                    NUMBER OF SEQUENCES: 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
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Length 30;
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TITLE OF INVENTION: No. US20030032075A1el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 100.0%; Score 139; DB 11; Best Local Similarity 100.0%; Pred. No. 3.1e-14; Matches 27; Conservative 0; Mismatches 0;
Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         015389-002931US
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                                                      PTLING DATE: 12-00-1999
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 36,429
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
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       12-NOV-1999
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; Publication No. US20030032075A1
; GENERAL INFORMATION:
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ADDRESSEE: Townsend and
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Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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Lingner, Joachim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1.30
CTHER INFORMATION:
CTHER INFORMATION:
US-09-438-486-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cech,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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APPLICANT: Cech, Thomas R.
APPLICANT: Lingmer, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US20030009019Alel Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                              CURRENT ARPLICATION DATA:

APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-3an-2001
CLASSIFICATION: UNKNOWN>
PRIOR APPLICATION: UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/846,017
FILING DATE: 199-04-25
APPLICATION NUMBER: US/846,017
FILING DATE: 01-0CT-1996
ATTORNEY/AGENT INPORMATION:
RAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELEPHONE: (415) 576-0300
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                        COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 139;
Best Local Similarity 100.0%; Pred. No. 3
Matches 27; Conservative 0; Mismatche
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; Sequence 167, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Peptide
LOCATION: 1..30
OTHER INFORMATION:
                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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Andrews, William H.

TITLE OF INVENTION: No. US20030059787A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                          NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 15;
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100.0%; Pred. No. 3.1e-14;
iive 0; Mismatches 0;
                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050
FILING DATE: «Uhrown»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: California
COUNTRY: United States of America
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             telomerase core protein 1 (TCP1)
SEQUENCE DESCRIPTION: SEQ ID NO: 167
US-10-054-295-167
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COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 167, Application US/10054611; Publication No. US20030059787A1; GENERAL INFORMATION:
                                                                                                           FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 167: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
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Lingner, Joachim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    roPoLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1.30
OTHER INFORMATION: /note= "motif 0 peptide from human telomerase core protein 1 (TCP1)"
SEQUENCE DESCRIPTION: SEQ ID NO: 167:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
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TITLE OF INVENTION: No. US20030044953A1el Telomerase
NUMBER OF SEQUENCES: 225
         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFRENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 15;
                                                                                                                                                                                      APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
APPLICATION NUMBER: US 08/846,017
FILING DATE: 05-MAY-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 139; 100.0%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 PALLTSRLRFIPKPDGLRPIVNMDYVV 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 167, Application US/10054295
Publication No. US20030044953A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Greeg B.
Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 27, Conservative
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Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE.OF INVENTION: HUMAN THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 30;
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COMPUTER: 1BM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Twomsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 139; DB 15; 100.0%; Pred. No. 3.1e-14;
                                                                          APPLICATION NUMBER: 08/854,050
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
FILING DATE: 18-APR-1997
FILING DATE: 01-0CT-1996
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COMPUTER READABLE FORM:
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APPLICATION NUMBER: US/10/044,692
APPLICATION NUMBER: US/10/054,611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         telomerase core protein 1 (TCP1);
SEQUENCE DESCRIPTION: SEQ ID NO: 167
US-10-054-611-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27
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Publication No. US20030096344A1
GENERAL INFORMATION:
                   FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: <Unknown:
                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 30 amino acids
                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 167
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
PEATURE:
                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: California
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Best Local Similarity 100..

Best Local 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
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Gaps
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OTHER INFORMATION: /note= "motif 1 and 2 peptide from
human TRT"
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                                                                                                                                                                                                                                                                                                                                          NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uvery Match 100.0%; Score 139; DB 15; Best Local Similarity 100.0%; Pred. No. 5.8e-14; Matches 27; Conservative 0; Mismatches
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951
FILING DATE: «Unknown»
APPLICATION NUMBER: 08 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAX-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 01-OCT-1966
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: November 12, 2003, 19:55:47 Job time : 21.566 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 31:
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                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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receptor-like tyro
coagulation factor
acetyl-CoA carboxy
conserved hypothet
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2-oxoglutarate/mal
hypothetical prote
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probable periplasm
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inositol 1,4,5-tri
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                                                                 November 12, 2003, 19:43:04; Search time 10.5283 Seconds (without alignments) 246.626 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                283308
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                               139
1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27
                                                                                                                                                                                                      283308 segs, 96168682 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                 Listing first 45 summaries
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S51605
T42763
T06600
AF2859
D97636
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G86369
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H64803
T31107
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F81171
A43857
S58738
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T01489
Q4ADAS
Q4ADA2
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D69230
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                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                    US-08-854-050-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
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Match Length
                                                                                                                                                                                                                                                                                                                                       PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                  Title:
Perfect score:
                                                                                                                                                                 Scoring table:
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                                                                     Run on:
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No.
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C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: C82255
R;Heidelberg J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Axture 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301

adenylate kinase VC0986 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

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Gaps

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Match 1132; Score 139; DB 2; Length 1132; Local Similarity 100.0%; Pred. No. 2.5e-13; les 27; Conservative 0; Mismatches 0; Indels 0

Query Match Best Loc Matches

1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27

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A;Cross-references: GB:AE004180; GB:AE003852; NID:g9655445; PIDN:AAF94147.1; GSPDB:GN00 A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics: A;Gene: VC0986 A;Map position: 1 C;Superfamily: adenylate Kinase

hypothetical prote pol protein - silk

D82538 C70876 T18196

45.

127976

polyphosphate kina protein - silk

hypothetical prote hypothetical prote

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-214 <HEI>

| 30 | 45 45 | 32.4 32.4 | | 00 | T44898 T00397 | |
|---------------------------------|--------------------|--|--|------------|--|---|
| 3 m | 4. 4. 7. 10. | 32.4 | 474 | 0 0 | T47699 T12536 | hypothetical prote |
| 34 | 45 | 32.4 | | 0 | D86565 | oligopeptide bindi |
| 35 | 45 | 32.4 | | 7 | E72059 | peptide ABC transp |
| 36 | 45 | 32.4 | | 7 | T15615 | hypothetical prote |
| 37 | 45 | 32.4 | | 0 | H86865 | hypothetical prote |
| 9 0 | 4. V. 1 | 32. | 291 | ~ | AB1384 | conserved hypothet |
| n (| 4. 4 V. 4 | 7.7 | | N (| AD1/59 | conserved hypothet |
| 0.5 | 4. 4. 4. V | 32.0 | 21.0 | N (| H97386 | hypothetical 32.0K |
| - · · | | | | ٧, | A12604 | Tysozyme limporred |
| 24. | 4.4 U | 3.0 | | - (| F70584 | phosphate specific |
| | 4. V. 1 | 32. | 544 | ~ (| A72459 | probable glutamyl- |
| * 4 * 8 | 44.5 | 32.0 | | 7 N | A84591 | triacyiglycerol ii 26S proteasome reg |
| | | | | | | |
| RESULT 1 T03844 | | | | | | |
| telomerase | se cata | lytic | catalytic chain - human | hum | | |
| N;Altern C:Specie | are nam a: Homo | es: te ganie | N,Alternate names: telomerase reverse C.Species: Homo saniens (man) | r. | verse transcriptase | |
| C;Date: | 23-Apr- | 1999 | seguence | re. | vision 23-Apr-1999 | C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999 |
| R:Nakamu | ra T M | MO | מי ני | | range A A canaca | C.Accessor. 100001: 100001: R.Nakamira, T.M. • Morin, G.R. • Chanman K.R.• Meinrich C.I. • Andrews M.D. • Lingner J. |
| Science 277, 955-959, 1997 | 277, 95 | 5-959, | 1997 | • | 1111 | |
| A; Title: | Telome | rase c | atalytic | su] | bunit homologs from | A; Title: Telomerase catalytic subunit homologs from fission yeast and human. |
| A Reference number: | nce num | | 215111; N | (UID | Z15111; MUID:97400623; PMID:9252327 | 2327 |
| A; Accession: T03844 | 10n: 10 | 3844 | | 1 | rand/ take/ ab | |
| A;Molecule type: mRNA | : preil | HILINGE) | /; craiisi | מ ה | Ajscacus: premiminary; cramsmaced from GB/EMBL/DDBU A;Molecule type: mRNA | |
| A; Residues: 1-1132 <nak></nak> | es: 1-1 | 132 <n< td=""><td>AAK></td><td></td><td></td><td></td></n<> | AAK> | | | |
| A; Cross- | referen mental | ces: 1 source | A;Cross-references: EMBL:AF01 A;Experimental source: kidney | 595 | 0; NID:92330016; PI | A,Cross-references: EMBL:AF015950; NID:g2330016; PIDN:AAC51672.1; PID:g2330017 A,Experimental source: kidney |
| A;Genetics: | cs: TRT | | | | | |
| A, Map position: | sition: | Sp | | | | |
| | | | | | | |

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C;Complex: acetyl-CoA carboxylase is composed of biotin carboxylase (EC 6.3.4.14), carb
C;Function: <ACC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Function: <BCC.

A.Description: blotin carboxyl carrier chain is responsible for binding of biotin

A.Perlway: farty acid biosynthesis

C.Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology

C.Superfamily: biotin metaboxilsm; holoroplast; farty acid biosynthesis; ligase

F.1-47/Domain: transit peptide (chloroplast) #status predicted <TNP.

F.48-262/Product: acetyl-CoA carboxylase, biotin carboxyl carrier chain #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein Atu2303 [imported] - Agrobacterium tumefaciens (strain C C,Species: Agrobacterium tumefaciens C,Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cjaccession: AF2859
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Description: entire acety1-CoA carboxylase complex catalyzes synthesis of malony1-CoA carboxylation of biotin bound to biotin-carboxyl-carrier protein with bicarbonate; car
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GB: AE008688; PIDN: AAL43292.1; PID:g17740782; GSPDB: GN00186
                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U40666; NID:g1143318; PIDN:AAB67836.1; PID:g1143319
A;Experimental source: strain Resnik
                        C;Species: Glycine max (soybean)
C;Species: Glycine max (soybean)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-Jan-2002
C;Accession: T06600
R;Nielsen, N.C.; Reverdatto, S.V.; Beilinson, V.A.
submitted to the EMBL Data Library, November 1995
A;Reference number: 215788
A;Reference number: 215788
A;Reference number: Common GB/EMBL/DDBJ
A;Reference number: Aranalated from GB/EMBL/DDBJ
A;Reference number: L262 «NIE»
A;Residues: 1-262 «NIE»
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N; Contains: biotin carboxyl carrier chain
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215 LPLIPEGPGNRPIIAMDY
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Matches 10; Conserv
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A; Residues: 1-327 < KUR>
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A,Gene: accB-1
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Oncogene 8, 3277-3288, 1993
A;Title: Ehk.1 and Ehk-2: two novel members of the Eph receptor-like tyrosine kinase fam
A;Reference number: S49015; MUID:94067777; PMID:7504232
A;Accession: S51605
A;Accession: Speloininary
A;Accession: Preliminary
A;Molecule type: mRNA
A;Residues: 1-948 <MAI>
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A; Residues: 1-2133 <LOLD:
A; Croser-references: EMBL:149517; NID:g1511633; PID:g1511634; PIDN:AAB06705.1
C; Cyperfamily: coagulation factor VIII; discoidin I amino-terminal homology; ferroxidase
C; Keywords: acute phase; blood coagulation; duplication; glycoprotein; hemophilia A; pla
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 20-2133/Product: coagulation factor VIII #status predicted <MAT>
F; 23-349/Domain: ferroxidase repeat homology <FOX1>
F; 402-730/Domain: ferroxidase repeat homology <FOX2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:S68030
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
C;Keywords: ATP; transmembrane protein
F;628-936/Domain: protein kinase homology <KIN>
F;636-644/Region: protein kinase ATP-binding motif
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                         C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 29-May-1998
C;Accession: S51605
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                                  DB 2; Length 214;
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Pred. No. 38;
2; Mismatches 1; Indels
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                                                                                          7; Indels
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A;Accession: T42763
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.7%; Score 51; DB 2;
larity 52.4%; Pred. No. 14;
Conservative 4; Mismatches
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                                                                                          6; Mismatches
                                  Score 52.5;
Pred. No. 1.
                                                                                                                                                                                       3 LLTSRLRFIPKPDGLRPI-VNMDYVV 27
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72.7%;
                               37.8%;
                  Ouery Match
Best Local Similarity 46.29
Matches 12; Conservative
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Best Local Similarity 72...
8; Conservative
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hes 11; Conserv
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|PFFIATLLYFLGAPDGLRP 29
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Best Local Similarity 48.09
Matches 12; Conservative
Query Match 35.3
Best Local Similarity 50.0
Matches 10; Conservative
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                                                                                                               Rigodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 232-2328, 2001
A.Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUID:2160851; PMID:11743194
A; Accession: D97636
A; Scession: D97636
A; Scession: D97636
A; Scession: Company
A; Wolecule type: DNA
A; Residues: 1-327 < KUR>
A; Wolecule type: DNA
A; Residues: 1-327 < KUR>
A; Wolecule type: DNA
A; Residues: cfetences: GB:AE007869; PIDN:AAK88045.1; PID:g15157467; GSPDB:GN00169
A; Map position: circular chromosome
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R;De Smedt, H.; Missiaen, L.; Parys, J.B.; Bootman, M.D.; Mertens, L.; Van Den Bosch, L.
Biol. Chem. 269, 21691-21698, 1994
A.Title: Determination of relative amounts of inositol trisphosphate receptor mRNA isofc A; Reference number: A53854; MUID:94342363; PMID:8063813
A; Accession: 148607
A; Accession: 148607
A; Accession: I48607
A; Residues: 1-409 < RES>
A; Cross_references: EMBL:233908; NID:9512565; PIDN:CAA83957.1; PID:9512566
C; Superfamily: inositol-trisphosphate receptor
                probable secreted protein AGR C 4189 [imported] - Agrobacterium tumefaciens (strain C58, C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
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R.Suedhof, T.C.; Newton, C.L.; Archer III, B.T.; Ushkaryov, Y.A.; Mignery, G.A. BEBO J. 10, 3199-3206, 1991
A.Title: Structure of a novel InsP(3) receptor.
A;Reference number: 817796, MUID:92007769; PMID:1655411
A;Accession: 817796
A;Cross-references: EMBL:X61677; NID:956507; PIDN:CAA43852.1; PID:956508
C;Superfamily: inositol-trisphosphate receptor
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inositol 1,4,5-trisphosphate receptor type 5 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 20-Aug-1999
C;Accession: I48607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inositol-trisphosphate receptor type 2 - rat
N/Alternate names: inositol-1,4,5-triphosphate receptor type 2
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
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2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.3%; Score 49; ilarity 55.6%; Pred. No. 8 Conservative 2; Mismatch
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Pred. No. 1
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215 LPLIPEGPGNRPIIAMDY 232
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Best Local Similarity 50.0%;
Matches 10; Conservative
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les 10; Conserv
                                                                                            Accession: D97636
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Matches
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RESULT 12

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Gracesion: G86369
RiTheologis, A.; Becker, J.R.; Palm, C.J.; Federapiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession. G64537

R;Tomb, J.F.; White, O; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenn

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

A;Reference number: A64520; MUID:97394467; PMID:9252185
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                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F508.15 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
                                                                           Gaps
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35.3%; Score 49; DB 2; Length 2701;
50.0%; Pred. No. 1e+02;
ive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 461;
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Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 2;
Pred. No. 7.7;
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A;Cross-references: GB:AE000511; TIGR:HP0143
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                                                                                                                                                                                                              2272 AICTSMLFFFSKPVGIRPFL 2291
                                                                                                                                          2 ALLTSRLRFIPKPDGLRPIV 21
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Gaps

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6; Indels

3; Mismatches

Score 47; DB 2; Length 1132; Pred. No. 75;

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probable periplasmic protein NVAO881 [imported] - Neisseria meningitidis (strain 22491 C; Species: Neisseria meningitidis (C; Species: Neisseria meningitidis (C; Species: Neisseria meningitidis (C; Species: Neisseria meningitidis (C; Species: Os May-2000 #text_change 02-Feb-2001 C; Accession: D81934 (S; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; More Narkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; More Nature 404, 502-506, 2000 (S; Moule, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream Nature 404, 502-506, 2000 (S; Mulb:20222556; PMID:10761919)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-203 <PAR>
A;Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84161.1; PID:g73795
A;Experimental source: serogroup A, strain 22491
C;Genetics:
                           A;Residues: 1-1132 <BRY>
A;Cross-references: EMBL:AF060230; NID:g3342795; PID:g3342796; PIDN:AAC39163.1
C;Genetics:
A;Gene: TERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.5%; Score 46.5; DB 2; Length 203; 41.7%; Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                      617 KLRLIPKGDTFRPIMTFN 634
                                                                                                                                                                                                                                                                                                 7 RLRFIPKPDGLRPIVNMD 24
                                                                                                                                                                           33.8%;
50.0%;
                                                                                                                                                                           Query Match
Best Local Similarity 50.09
Matches 9; Conservative
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Matches 10; Conserv
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A; Molecule type: DNA
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Job time
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C;Species: Oxytricha trifallax
C;Species: Oxytricha trifallax
C;Date: O2-Sep-2000 #sequence_revision O2-Sep-2000 #text_change O2-Sep-2000
C;Accession: T31107
R;Bryan, T.M.; Sperger, J.M.; Chapman, K.B.; Cech, T.R.
Proc. Natl. Acad. Sci. U.S.A. 95, 8479-8484, 1998
A;Title: Telomerase reverse transcriptase genes in Tetrahymena thermophila and Oxytricha
A;Reference number: Z20985; MUID:98337940; PMID:9671703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession. H64803

C;Accession. H64803

C;Blatener, F.R., Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cd

A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-164 <BLAT>
A;Cross-references: GB:ME000172; GB:U00096; NID:g1786896; PIDN:AAC73783.1; PID:g1786905;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
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                                                                                                                                                                    A;Reference number: 219923
A;Reference number: 219923
A;Reference number: 219923
A;Accession: 124685
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rocelus: preliminary; translated from GB/EMBL/DDBJ
A;Reference: EMBL: 250756; PIDN: CAA90637.1; GSPDB:GN00028; CESP:T08D10.2
A;Experimental source: clone T08D10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: CESP:T08D10.2
A;Map position: X
A;Introns: 43/2; 64/1; 135/1; 272/3; 301/1; 345/2; 379/2; 520/1; 586/2; 643/2
C;Superfamily: Caenorhabditis elegans hypothetical protein Y40B1B.6
                     hypothetical protein T08D10.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ybfP protein - Escherichia coli (strain K-12)
NiAlternate names: protein b0689
C.Species: Escherichia coli
C.Spate: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 34.5%; Score 48; DB 2; Length 803; Best Local Similarity 66.7%; Pred. No. 34; Matches 10; Conservative 1; Mismatches 4; Indels
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Pred. No. 6.1;
0; Mismatches 2;
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ilarity 78.6%;
Conservative (
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Best Local Similarity
Matches 11; Conserv
                                                                                                                      Accession: T24685
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Gaps

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Indels

6; Mismatches

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November 12, 2003, 19:41:59 ; Search time 5.60377 Seconds (without alignments) 226.583 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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127863 US-08-854-050-117 139 1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27 127863 seqs, 47026705 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Scoring table: Sequence: Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| SUMMARIES | TERT HUMAN TERT_MOUSE EPAG_ EAD VIBCH EPAG PIG BOCD SOVEN BOCD SOVEN BOCD SOVEN BOCD SOVEN BOCD SOVEN TERT OXYTR TERT OXYTR BOLD SERVE SOVEN TERT OXYTR BOLD SERVE SOVEN TERT OXYTR BOLD SERVE SOVEN TERT OXYTR TOXYTR SOVEN TERT OXYTR TOXYTR TOXYTR TOXYTR SOVEN TERT OXYTR TOXYTR TOXYT | ı |
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| Score | 0.0 444 44444 4444 60 60 60 60 60 60 60 60 60 60 60 60 60 | |
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| Q8zyx2 pyrobaculum O52512 streptomyce | Q59284 corynebacte P43283 zea mays (m Q16797 drosophila | P03273 human adeno P14726 hordeum vul | O51345 borrelia bu O74991 schizosacch | Q53176 rhodobacter O8r8z8 rhermoanser | щ |
|--|---|--|---------------------------------------|--|------------|
| TRPC_PYRAE T2S1_STRFI | DAPE_CORGL TRP1_MAIZE RL3_DROME | PIVZ ADE07 UFOG HORVU | SYE BORBU POF3 SCHPO | NAPA_RHOSH Y134_THETN | CLPX_BACSU |
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| 249 | 369 389 415 | 448 455 | 490 577 | 831 | 420 |
| 30.9 | 30.9 9.08 9.09 | 30.9 | 30.9 30.9 | 30.9 | 30.6 |
| 4.4 8.3 | 4 4 4 E E E | 4 4 3 | 43 43 | 42.5 | 42.5 |
| 3.4 3.5 | 36 37 38 | 39 | 417 | 4. 4. E. 4. | 45 |

ALIGNMENTS

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16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA-binding
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        SO THE REPORT OF THE PROPERTY AND THE PR
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005696; C:telomere; TAS.
GO; GO:0003721; F:telomeric template RNA reverse transcriptas. . .; TAS.
GO; GO:0007031; P:telomere binding; TAS.
InterPro; IPR000477; RVIse.
InterPro; IPR003545; Telomerase_RT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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-!- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01365; TELOMERASERT.
Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Telomerase reverse transcriptase (BC 2.7.7.-) (Telomerase catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98241176; PubMed=9582020;
Greenberg R.A., Allsopp R.C., Chin L., Morin G.B., DePinho R.A.;
"Expression of mouse telomerase reverse transcriptase during
development, differentiation and prolliferation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98393668; PubMed-9724727;
Martin-Rivera L., Herrera E., Albar J.P., Blasco M.A.;
"Expression of mouse telomerase catalytic subunit in embryos and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 1132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              516 516 D -> G (IN REF. 2).
1132 AA; 126996 MW; 94E35469C4CA33A0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.0%; Pred. No. 8e-14; nes 27; Conservative 0; Mismatches
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                                                                                                                                                                                                                  EMBL; AF018167; AAC51724.1; -.
EMBL; AF128894; AAD30037.1; -.
EMBL; AR128893; AAD30037.1; JOINED.
EMBL; AX007685; AAG3289.1; -.
PIR; T03844; T03844.
Genew; HGNC:11730; TERT.
                                                                                                                                                                                      EMBL; AF015950; AAC51672.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI TaxID=10090;
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070372; 035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20406833, PubMed=10952301;
MEDLINE=20406833, PubMed=10952301;
Meidelboerg J.F., Bisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
SUBUNIT: Inceracts with PINX1 (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
TELOMERASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR01365; TELOMERASERT.
Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "DNA sequence of both chromosomes of the cholera pathogen Vibrio
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-!- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR MAINTENANCE AND CELL GROWTH.

-!- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
-!- SUBMIT: MONOMER (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUMCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the adenylate kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 66.9%; Score 93; DB 1; Length 1122; Local Similarity 75.0%; Pred. No. 1.5e-06; Les 18; Conservative 2; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 I -> V (IN REF. 3).
127977 MW; F85266905DD6558C CRC64;
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InterPro; IPR003545; Telomerase_RT.
Pfam; PF00078; rvt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF051911; AAC09323.1; -.-
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF073311; AAC34821.1; -. EMBL; AF029235; AAB84200.1; -.
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NCBI_TaxID=666;
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Vibrio cholerae
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SEQUENCE OF 392-759 FROM N.A.
                  Pfam; PF00069; pkinase; 1.
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409
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SEQUENCE
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STRAINS SPROAGE TOWN 1.7.

WEDLINE 94067777; PubMed=7504232;

Majsompleter B.C.

Majsompleter B
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Ephtin type-A receptor 6 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor EHK-2) (EPH homology kinase-2) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.8%; Score 52.5; DB 1; Length 214; 46.2%; Pred. No. 0.59; 7; Indels 1
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SEQUENCE 214 AA; 23276 MW; D7600C1DC0A3E95B CRC64;
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PRINTS; PRODOS4; ADENYLTKNASE.
PEODOM; PD000657; Adenylate kin; 1.
TIGRFAMS; TIGR01351; adk; 1.
PROSITE; PS00113; ADENYLATE KINASE; 1.
Transferase; Kinase; ATP-binding; Complete proteome.
NP BIND
7 15 ATP (BY SIMILARITY)
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PIR; C82255; C82255.
HSSP; P05082; JAKE.
TIGR, VC0986; -.
HAMAP; MF 00235; -; 1.
InterPro; IPR0006259; Adenylate kin.
Pfam; PF00406; ADK; 1.
Pfam; PF00191; ADK 11d; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0uery Match
Best Local Similarity 46.27
Matches 12, Conservative
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P54758;
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PRINTS; PROUDOS; ALAIMENE; 1.

PRINTS; PROUDOS; TYRKINASE.

PRINTS; PROUDOS; TYRKINASE.

PRODOM; PD001095; EPH IDG; 1.

RMART; SM00109; TYRKINASE.

RMART; SM00109; TYRKIN, 1.

RMART; SM00109; TYRKIN, 1.

RPGSTTE; PS00100; PROTEIN KINASE ATP; 1.

RPGSTTE; PS00109; PROTEIN KINASE DOM; 1.

RPGSTTE; PS00790; RECEPTOR TYR KIN V 1; 1.

RPGSTTE; PS00790; RECEPTOR TYR KIN V 1; 1.

RPGSTTE; PS001186; EGF 2; UNKNOWN 1.

RRGSTTE; PS001186; EGF 2; UNKNOWN 1.

TRANSFERAS; TYCOSING-PROTEIN; KINASE, ATP-binding; Phosphorylation; SIGNAL

TRANSFERASE; TYCOSING-PROTEIN; SIGNAL; REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Proc. Natl. Acad. Sci. U.S.A. 83:5939-5942(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION (AUTO-) (POTENTIAL).
PHOSPHORYLATION (AUTO-) (POTENTIAL).
PHOSPHORYLATION (AUTO-) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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MEDLINE-86287369; PubMed=3016730;
TOOLE J.J., Pittman D.D., Orr E.C., Murtha P., Wasley L.C.,
Kaufman R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PA8 PIG STANDARD; PRT; 2133 AA.
101263; Q95243;
01-007-1999 (Rel. 12, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
Coagulation factor VIII precursor (Procoagulant component)
PR OR CRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 51; DB 1; Length 948; Pred. No. 5.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Healey J.F., Lubin I.M., Lollar P.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIBRONECTIN TYPE-III 1. FIBRONECTIN TYPE-III 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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l Similarity 52.4%;
ll; Conservative
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RESULT 6
BCCP_SOYBN STANDARD; PR1
1D BCCP_SOYBN STANDARD; PR1
20 404703;
DT 15-JUL-1998 (Rel. 36, Last sequer
DT 28-FEB-2003 (Rel. 41, Last annote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, U40666; AAB67836.1; -.
PIR, T06600; T06600.
HSSP; P02905; 3BDO.
                                                                                                                                                                                                                 36.78;
                                                                                                                                                                                      239304
                                                                                                                                                                                                                             72.78;
                                                                                                                                                                                                                               Local Similarity 72.7
es 8; Conservative
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612 RFLPNPDGLQP 622
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1408
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                            CARBOHYD
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  CARBOHYD
              CARBOHYD
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                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLASTOCYANIN-LIKE 5.
PLASTOCYANIN-LIKE 6.
FS/8 TYPE C 1.
FS/8 TYPE C 2.
CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
CLEAVAGE (ACTIVATION) (BY SIMILARITY).
CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
SULFATION (BY SIMILARITY).
PROBABLE.
PROBABLE.
PROBABLE.
             Lubin I.M., Healey J.F., Scandella D., Runge M.S., Lollar P.,
"Elimination of a major inhibitor epitope in factor VIII.";
J. Biol. Chem. 269:8659-8641 (1994).
-!- Biol. Chem. 269:8659-8641 (1994).
-!- PUNCTION: EACTOR VIII. ALONG WITH CALCIUM AND PHOSPHOLIPID, ACTS
AS A COPACTOR FOR PACTOR IXA WHEN IT CONVERTS FACTOR X TO THE
ACTIVATED FORM, FACTOR XA.
-!- SUBCELbullar LOCATION: Extracellular.
-!- SIMILARITY: Contains 3 F5/8 type A domains.
-!- SIMILARITY: Contains 2 F5/8 type C domains.
-!- SIMILARITY: STRONG, TO COAGULATION FACTOR V.
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##SEP: P00451; 14605.

##BEP: P00451; 176001117; Cu-oxidase.

##BEP: P00451; 176001117; Cu-oxidase.

##BEP: P00454; FU-Oxidase.

##BEP: P00344; FU-Oxidase.

##BEP: P00344; FU-Oxidase.

##BEP: P00321; FASEC.

##BEP: PS01285; FASEC.

##BEP: PS01285; FASEC.

##BEP: PS01285; FASEC.

##BEP: PS01285; FASEC.

##BEP: PS00221; FASEC.

##BEP: PS00221;
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PLASTOCYANIN-LIKE 2.
FS/8 TYPE A 2.
PLASTOCYANIN-LIKE 3.
PLASTOCYANIN-LIKE 4.
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BY SIMILARITY.

N-LINKED (GLCNAC.)

N-LINKED (GLCNAC.)
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-LINKED
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  MEDLINE=94179260; PubMed=7510693
                                                                                                                                                                                                                                                                                         EMBL; U49517; AAB06705.1; -.
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PIR; T42763; T42763.
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STRAIN-cv. Resnik;
Reverdatto S.V., Beilinson V., Neilsen N.C.;
Reverdatto S.V., Beilinson V., Neilsen N.C.;
Contaracterization of a cDNA clone encoding a BCCP subunit of acetyl-coa carboxylase from soybean...;
(In) Plant Gene Register PGR96-040.
-!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES THE CARBOXYLATION OF THE CARBOXYLASE CATALYZES THE TRANSCARBOXYLASE TRANSCARBOXYLASE TRANSCARBOXYLASE
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28-FEB-2003 (Rel. 41, Last annotation update)
Biotin carboxyl carrier protein of acetyl-CoA carboxylase, chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycine max (Soybean).
Glycine max (Soybean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosida eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                   (POTENTIAL)
                                                                                   (POTENTIAL) (POTENTIAL)
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InterPro; IPR011842; Biotin attach.
InterPro; IPR001089; Biotin attach.
InterPro; IPR001089; Biotin lipoyl.
Pfam; PF00364; biotin lipoyl; 1.
PRINTS; PR01071; ACOABIOTINCC.
ITGREAMS; TIGR00531; BCCP; 1.
PROSITE; PS00188; BIOTIN; 1.
PROSITE; PS00188; Biotin; Chloroplast; Transit peptide.
TRANSIT

    -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.
    -!- SUBCELLULAR LOCATION: Chloroplast.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 51; DB 1; Length 2133;
Pred. No. 14;
N-LINKED (GLCNAC. . .) (POTENY N-L) (G-S) (IN REF. 2) (G-S) (IN REF. 2) (G-S) (IN REF. 2) (G-S) (G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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                                                                                                                                                                      IP35 MOUSE STANDARD; PRT; 1281 AA.
092329; P70226; Q61744;
092329; P70226; Q61744;
28-FEB-2003 (Rel. 41, Last sequence update)
15-FEB-2003 (Rel. 42, Last annotation update)
11008itol 1,4,5-trisphosphate receptor type 2 (Type 2 inositol 1,4,5-trisphosphate receptor type 2 (Type 2 inositol 1,4,5-trisphosphate receptor) (IP3 receptor isoform 2) (InsP3R2) (Inositol 1,4,5-trisphosphate type V receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-TERMINAL EXTREMITY. ITS LARGE N-TERMINAL CYTOPLASMIC REGION HAS THE LIGAND-BINDING SITE IN THE N-TERMINUS AND MODULATORY SITES IN THE MIDDLE PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Short; Synonyms=TIPR;
IsoId=092329-2; Sequence=VSP_002701, VSP_002702;
TISSUE SPECIFICITY: THE SHORT ISOFORM IS FOUND IN SKELETAL MUSCLE
                                                                            Gaps
                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97218118; PubMed=9065779;
De Smedt H., Missiaen L., Parys J.B., Henning R.H., Sienaert I., Vanlingen S., Gijsens A., Himpens B., Casteels R.;
Isoform diversity of the inositol trisphosphate receptor in cell types of mouse origin.";
Biochem. J. 322:575-583(1997).
  PROTEIN OF
                                                                            ..
0
                                                     35.3%; Score 49; DB 1; Length 262; 66.7%; Pred. No. 2.7;
                                                                            4; Indels
BIOTIN CARBOXYL CARRIER PR
ACETYL-COA CARBOXYLASE.
BIOTIN (BY SIMILARITY).
79B273BD8B87DF48 CRC64;
                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-272 FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reticulum (By similarity).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isold=Q9Z329-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                    TISSUE=Heart;
MEDLINE=98399819; PubMed=9729462;
                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 273-1281 FROM N.A. STRAIN=C3H; TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 818-1226 FROM N.A.
                                27657 MW;
                                                                                               4 LTSRLRFIPKPDGLR 18
                                                                                                              || || || || || || || || LTHSLRFSPKPNNLR 31
                                                                          Conservative
                    227
                    227 2
262 AA;
                                                               Local Similarity
les 10; Conserv
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
 48
                                                                                                                                                                                                                                                                          ITPR2 OR ITPR5.
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                                SEQUENCE
                                                      Query Match
                    BINDING
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                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00520; ion trans; 2.
Pfam; PF002815; MRR; 1.
SMART: SM040472; MRR; 1.
Receptor; Transmembrane; Glycoprotein; Phosphorylation;
Endoplasmic reticulum; Ionic channel; Ion transport; Calcium channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Inositol 1,4,5-trisphosphate receptor type 2 (Type 2 inositol 1,4,5-trisphosphate receptor 1 Inositol 1,4,5-trisphosphate receptor)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
PTM: PHOSPHORYLATED ON TYROSINE RESIDUES (BY SIMILARITY). SIMILARITY: BELONGS TO THE INSP3 RECEPTOR FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAE789986E9A5598 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Missing (in isoform Short).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (POTENTIAL)
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3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
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MEDLINE=94363219; Pubmed=8081734;
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Local Similarity 50.0%;
Local Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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Q14571; O94773;
01-NOV-1997 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                             Futering A., Kuwajima G., Mikoshiba K.;

"Muscle-specific mRNA isoform encodes a protein composed mainly of the N-terminal 175 residues of type 2 Ins(1,4,5)P3 receptor.";

Biochem. J. 334:559-563(1998)

-- FUNCTION: RECEPTOR FOR INOSITOL 1,4,5-TRISPHOSPHATE, A SECOND MESSENGER THAT MEDIATES THE RELEASE OF INTRACELLULAR CALCIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN: THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-TERMINAL BEXTREMITY. ITS LARGE N-TERMINAL CYTOPLASMIC REGION HAS THE LIGAND-BINDING SITE IN THE N-TERMINUS AND MODULATORY SITES IN THE LIGAND-PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL REGION.

PTM: PHOSPHORYLATED ON TYROSINE RESIDUES (BY SIMILARITY).

MISCELLANBOUS: CALCIUM APPEARS TO INHIBIT LIGAND BINDING TO THE RECEPTOR, MOST PROBABLY BY INTERACTING WITH A DISTINCT CALCIUM-BINDING PROPER WHICH THEN INHIBITS THE RECEPTOR.

SIMILARITY: BELONGS TO THE INSP3 RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISOId=Q14571-2; Sequence=VSP 002699, VSP 002700;
TISSUE SPECIFICITY: THE SHORT ISOFORM IS FOUND IN SKELETAL MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 600144; -.
60; 602783; C:endoplasmic reticulum; TAS.
60; 60305783; C:plasma membrane; TAS.
60; 60:0005886; C:plasma membrane; TAS.
60; 60:0015085; F:calcium ion transporter activity; TAS.
60; 60:000165; F:signal transporter activity; TAS.
60; 60:0007165; P:signal transduction; TAS.
60; 60:000832; P:signal transport; TAS.
InterPro; IPR001682; Ca_rel_channel.
InterPro; IPR001682; Ca_rel_channel.
InterPro; IPR001682; Ion_trans.
InterPro; IPR001682; Ion_trans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor; Transmembrane; Glycoprotein; Phosphorylation;
Endoplasmic reticulum; Ionic channel; Ion transport; Calcium channel;
Yamamoto-Hino M., Sugiyama T., Hikiti K., Mattei M.-G., Basegawa K., Sekine S., Sakurada K., Miyawaki A., Furuichi T., Hasegawa M., Mikoshiba K.; Cloning and characterization of human type 2 and type 3 inositol
                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: Homotetramer (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q14571-1; Sequence=Displayed;
Name=Short; Synonyms=TIPR;
IsoId=Q14571-2; Sequence=VSP_002699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM SHORT).
                                                                                                                                                                                                               MEDLINE=98399819; Pubmed=9729462;
                                                                                            1,4,5-trisphosphate receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB012610; BAA33961.1; -.
                                                                                                                  Recept. Channels 2:9-22(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D26350; BAA05384.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00520; ion trans; 1. Pfam; PF02815; MIR; 4. Pfam; PF01365; RYDR ITPR; 2. SMART; SM00472; MIR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:6181; ITPR2.
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TRANSMEM
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TRANSMEM
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01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Inositol 1,4,5-trisphosphate receptor type 2 (Type 2 inositol 1,4,5-trisphosphate receptor) (Type 2 InsP3 receptor isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reticulum.

DOMAIN: THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-TERMINAL EXTREMITY. ITS LARGE N-TERMINAL CYTOPLASMIC REGION HAS THE LIGAND-BINDING SITE IN THE N-TERMINUS AND MODULATORY SITES IN THE MIDDLE PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL RESIOUS. PTM: PHOSPHORYLATED ON TRROSINE RESIDUES (BY SIMILARITY).

SIMILARITY: BELONGS TO THE INSP3 RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukāryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Magnino F., Dufour J.F.;

"New rat IP3R isoform 2 sequence.";
"New rat IP3R isoform 2 sequence.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: RECEPTOR FOR INOSITOL 1,4,5-TRISPHOSPHATE, A SECOND
MESSENGER THAT MEDIATES THE RELEASE OF INTRACELLULAR CALCIUM.
                                                                                                                      CYTOPLASMIC (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
IVVGDK -> DASFWI (in isoform Short).
FIIG-VSP_002699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                            Score 49; DB 1; Length 2701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Suedhof T.C., Newton C.A., Archer B.T. III, Ushkaryov Y.A.
Mignery G.A.;
                                                                                                                                                                                                                                                                                                                                                                                7; Indels
                                                                                                                                                                                                                                                                            MW; EB5C7DDCDD17F74A CRC64;
                                                                                                                                                                                                                        Missing (in isoform Short). / FTId=VSP 002700.
                                                                         EXTRACELLULAR (POTENTIAL).
                          CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2701 AA.
                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structure of a novel InsP3 receptor."; EMBO J. 10:3199-3206(1991).
                                                                                                    POTENTIAL.
                                                  POTENTIAL
POTENTIAL
                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2272 AICTSMLFFFSKPVGIRPFL 2291
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                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ALLTSRLRFIPKPDGLRPIV 21
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                                                                                                                                                                                                                                                                                  2701 AA; 308074
                                                                                                                                                                                                                                                                                                                                                                                   10; Conservative
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                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                         2543
2607
176
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13 KPDGLRPIVNMDYV 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YBFP OR B0689.
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P75737;
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SEQUENCE
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                                                                                                                                                   Receptor; Transmembrane; Phosphorylation; Endoplasmic reticulum; Ionic channel; Ion transport; Calcium channel; Polymorphism. DOMAIN 2227 CYTOPLASMIC (POTENTIAL).
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Pasteurellaceae; Actinobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 49; DB 1; Length 2701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42BF7F1024335984 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
PHOSPHORYLATION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CU1000;
MBDLINE-98295003; PubNed=9631542;
Kaplan J.B., Fine D.H.;
"Codan usage in Actinobacillus actinomycetemcomitans.";
"Codon usage in Lett. 163:31-36(1998).
-!- SIMILARITY: Belongs to the UPF0042 family.
                                                                                                                                                                                                                                                                            POTENTIAL.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical UPF0042 protein HI1146 homolog (Fragment).
Actinobacillus actinomycetemcomitans (Haemophilus
                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                          POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                InterPro; IPR000699; Ca-rel channel.
InterPro; IPR001682; Ca/Na_pore.
InterPro; IPR005821; Ion_trans.
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                                                                                Pfam; PF00520; ion trans; 1.
Pfam; PF02815; MIR; 4.
Pfam; PF01365; RYDR ITPR; 2.
SMART; SM00472; MIR; 4.
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50.0%;
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Best Local Similarity 50.0°
Matches 10; Conservative
                                                                     InterPro; IPR003608; MIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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2607
689
1013
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2384
2694
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344
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DORREL DORRER DO
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                                       noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
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Science 277:1453-1474(1997).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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STRAID=KIZ / MG1652,
STRAID=KIZ / MG1657;
Pubbled=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.9%; Score 48.5; DB 1; Length 110; 45.0%; Pred. No. 1.2; tive 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.2%; Score 47.5; DB 1; Length 164; 78.6%; Pred. No. 2.7; Live 0; Mismatches 2; Indels 1
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      institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                    110 110 110 110 110 AA; 12481 MW; EAESDF10D7547DB8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical lipoprotein ybfP precursor.
use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 AA
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EcoGene; EG14158; ybfP.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
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164 AA; 18282 MW;
                                                                                                                                                    EMBL; U89523; AAC46410.1; -. HAMAP; MF 00655; -; 1. InterPro; IPR005337; UPF0042. Pfam; PF03668; ATP bind2; 1. Hypothetical proteIn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 45.0
les 9; Conservative
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es 11; Conservative
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NCBI_TaxID=5803;
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                                                                                                                                         development.
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P42789;
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   SO WENT HE DESCRIPTION OF THE PROPERTY OF THE 
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X MEDLINE=22508454; PubMed=12620739;

A MAXINO K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

I ijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

A Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism

distinct from that of V. cholerae.",

Lancet 36:743-749(203).

Lancet 36:743-749(203).

- PUNCTION: This small ubiquitous enzyme is essential for

maintenance and cell growth.

- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.

- SUBUNIT: Monomer (By similarity).

- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

- SIMILARITY: Belongs to the adenylate kinase family.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annoration update)
C-terminal binding protein (TCF-3 co-repressor CtBP) (XCtBP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                           IS-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase)
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PROSITE; PS00113; ADENYLATE_KINASE; 1.
Transferase; Kinase; ATP-binding; Complete proteome.

Transferase; Thase; ATP-binding; Complete proteome.

15 ATP (BY SIMILARITY)
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                                                                                                                                                                                                             214 AA
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                                117 KP-GTRPIVNEDYV 129
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nes 12; Conservative
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                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrio parahaemolyticus.
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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SEQUENCE FROM N.A.
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Q9W758;
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Q87RH4;
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                                                                                                                                         RESULT 12
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Oocyst;
MEDLINE=9114914; PubMed=8426605;
MEDLINE=9114914; PubMed=8426605;
Abrahamsen M.S., Clark T.G., Mascolo P., Speer C.A., White M.W.;
Abrahamsen M.S., Clark T.G., Instead bovis.";
"Developmental gene expression in Eineria bovis.";
Mol. Biochem. Parasitol. 57:1-14(1993).
-!- FUNCTION: MAY BE INVOLVED IN THE DESRADATION OF A PROTEIN WHICH IS
                                                                                A COMPONENT OF THE SIGNAL TRANSDUCTION PATHWAY REGULATING OOCYST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
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                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE D-ISOMER SPECIFIC 2-HYDROXYACID DEHYDROGENASES FAMILY. BUT HIGHLY DIVERGENT.
MEDLINE=99307079; PubMed=10375506;
Brannon M., Brown J.D., Bates R., Kimelman D., Moon R.T.;
"XCtBP is a XTcf-3 co-repressor with roles throughout Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.8%; Score 47; DB 1; Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       437 AA; 47775 MW; 49D2FEFD82E2B010 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSFORCY TO 3243; -- ...
InterPro; IPR006139; 2-Hacid_DH.
InterPro; IPR006140; 2-Hacid_DH.C.
Pfam; PP02805; 2-Hacid_DH; 1.
PROSITE; PS00065; D_2 HYDROXYACID_DH 1; 1.
PROSITE; PS00670; D_2 HYDROXYACID_DH 1; 1.
PROSITE; PS00671; D_2 HYDROXYACID_DH 2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-RDS-2003 (Rel. 41, Last annotation update)
Sporozoite developmental protein (EC 3.4.99.-).
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF152006; AAD41370.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thermophila and Oxytricha trifallax.";

Proc. Natl. Acad. Sci. U.S.A. 95:8479-8484(1998).

-!- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT ELOMGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE SEQUENCE MITHIN THE RNA COMPONENT OF THE ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01365; TELOMERASERT. Transferase; Telomere; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Telomerase catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98337940; PubMed=9671703;
Bryan T.M., Sperger J.M., Chapman K.B., Cech T.R.;
"Telomerase reverse transcriptase genes identified in Tetrahymena
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NCBI_TaxID=5946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Nuclear SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY. TELOMERASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                          33.8%; Score 47; DB 1; Length 596; 43.5%; Pred. No. 14; vative 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                      4BF9A9B17B358AA0 CRC64;
                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                           ZINC (BY SIMILARITY)
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30-WAY-2000 (Rel. 39, Last annotation update)
Telomerase reverse transcriptase (EC 2.7.7.)
subunit) (Telomerase subunit Pl33).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              320 LAKRLELLGLADGLSPVVDKNTV 342
                                                                                                                                                                                         InterPro; IPR001431; Peptidase M16.
Pfam; PF00675; Peptidase M16; I.
Pfam; PF05193; Peptidase M16_C; I.
PROSTIR; PS00143; INSULINASE; I.
Hydrolase; Metalloprotease; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LTSRLRFIPKPDGLRPIVNMDYV 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003545; Telomerase_RT.
                                                                                                                                                       EMBL; M98842; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                65279 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF060230; AAC39163.1; -. PIR; T31107; T31107.
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                                                                                                                                                                                                                                                                                                                                                                    596 AA;
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                       MEROPS; M16.UPA; -
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Gaps
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                                               Score 47; DB 1; Length 1132;
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               1132 AA; 134124 MW; 81E145F5F24392DC CRC64;
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                                                              Pred. No.
                                                                                                                                         617 KLRLIPKGDTFRPIMTFN 634
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                                               33.8%;
50.0%;
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Best Local Similarity 50.0
Matches 9; Conservative
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DNA-binding.
SEQUENCE
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Seguence:

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Searched:

Database

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Hisatomi H., Nagao K., Kanamaru T., Hirata H., Miyachi K., Hikiji H.;
Hisatomi H., Nagao K., Kanamaru T., Hirata H., Miyachi K., Hikiji H.;
Hisatomi II deleted variant of human reverse transcripatse.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB086550; BAC11015.1;
InterPro; IPR003545; Telomerase_RT.
InterPro; IPR05545; Telomerase_RT.
FRNA-directed DNA polymerase.
SEQUENCE 795 AA; 88965 MW; 6BBACBACDIAZEBCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
ABG-deleted variant of telomerase reverse transcriptase.
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Pred. No. 5.5e-13;
Migmatches 0;
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09LQC3
09LQC3
09LNP9
09CS98
08RCK8
09ASG1
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08D15
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09C0D2
09C0D2
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P95814
Q8VBS5
Q8SSU8
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01-OCT-2002 (TrEMBLrel. 22, Created)
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Best Local Similarity 100.0%;
Matches 27; Conservative 0
  PRELIMINARY;
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(Human)
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TISSUE=Stomach;
 NCBI_TaxID=9606;
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 Q8NG38
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ID Q8
AC Q8
DT 01
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Q8n6c3 homo sapien
Q8ng46 homo sapien
Q9gxz4 mesocricetu
Q9jk99 rattus norv
Q9de32 xenopus lae
Q96ZF9 cryptospori
Q8n23 fischerella
Q8n13 oryza sativ
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Ogud25 agrobacteri
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Q9grc5 paramecium
Q8muq8 paramecium
                                                                                    2003, 19:42:29 ; Search time 25.8113 Seconds (without alignments) 269.937 Million cell updates/sec
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            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                1 PALLTSRLRFIPKPDGLRPIVNMDYVV 27
                                                                                                                                                                                                                               830525 seqs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
                                                             OM protein - protein search, using sw model
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QBNG46
QBNG46
Q9QXZ4
Q9DE32
Q9DE32
Q9CX23
Q9CX23
Q9CX23
Q9CX23
Q9CX23
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sp_bacteria:*
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sp_organelle:*
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Gaps

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Result Š

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SEQUENCE FROM N.A. MEDLINE=21240330; PubMed=11342218; MEDLINE=21240330; PubMed=11342218; Guo W., Okamoto M., Lee Y.M., Baluda M.A., Park N.H.; "Enhanced activity of cloned hamster TERT gene promoter in transformed activity of cloned hamster TERT gene promoter in transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 100; DB 11; Length 1128;
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66.9%; Score 93; DB 11; Length 575;
Best Local Similarity 75.0%; Pred. No. 6.1e-06;
Matches 18; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochim. Biophys. Acta 1517:398-409(2001).

EMBL; AF149012; AAF17334.1; -
InterPro; IPR00347; RVISe.
InterPro; IPR003545; Telomerase_RT.

Pfam; PF00078; rvt; 1.

PRINTS; PR01365; TELOMERASERT.

RNA-directed DNA polymerase; Transferase.

SEQUENCE 1128 AA; 128394 MW; 1D4F81249012174E CRC64;
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"Rat Letomerase catalyric subunit, rTERT.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF247818; AAF62177.1;
-InterPro; IPR00047; RVTse.
InterPro; IRR003545; Telomerase_RT.
Pfam; PP00078; rvt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  575 AA; 65672 MW; F80C81BD7F6A91A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
101-mar-ase reverse transcriptase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1e-06;
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Best Local Similarity 73.1%; Pred. No. 15.
Matches 19; Conservative 2; Mismatches
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RNA-directed DNA polymerase; Transferase.
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01-OCT-2000 (TrEMBLrel. 15, Last sequenc)
01-OCT-2002 (TrEMBLrel. 22, Last annotation of the contact of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             608 PAMPICRLRFIPKPSGLRPIVNMSYM 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 PALLTSRLRFIPKPDGLRPIVNMDYV 26
(Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ALLTSRIRFIPKPDGLRPIVNMDY 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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Mesocricetus auratus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                             NCBI_TaxID=10036;
                                                                                                                        Mesocricetus
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Q9DE32;
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                                                                                                                                                                                                                                                                                                                                                                                                         cells."
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Q9JK99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hisatomi H., Nagao K., Kanamaru T., Sumida H., Hirata H., Yamamoto M.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kazumasa H.;
"Both beta and gamma deletion isoform of human telomerase reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 139; DB 4; Length 807; 100.0%; Pred. No. 5.6e-13;
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Hisatomi H., Nagao K., Hirata H., Hikiji K., Kanamaru T.;
"Exon 11 deleted variant of the human telomerase reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcriptage.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB086379; BAC11014.1; -.
InterPro; IPR003545; Telomerase_RT.
PRINTS; PR01365; TELOMERASERT.
SEQUENCE 807 AA; 90225 MW; 199664460CE6D763 CRC64;
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EMBL, AB085628; BAC11010.1; -.
InterPro; IPR003545; Telomerase_RT.
PRINTS; PR01365; TELOMERASERT.
RNA-directed DNA polymerase.
SEQUENCE 1069 AA; 120047 MW; BEIE77A653BIC666 CRC64;
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Beta and gamma deletion isoform of telomerase reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Telomerase catalytic subunit.
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HTERT.
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Best Local Similarity 100.v.,
Local 27; Conservative
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Matches 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Stomach cancer;
                                                                                                                                                                                                      Homo sapiens (Human)
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Q8NG46; **08NG46**

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SEQUENCE FROM N.A.

Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,

Harris B., Lennard N., Hall N., Arkin R., Chillingworth C., Doggett J.,

Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.;

Submitted (SEP-2002) to the BBL/GenBank/DDBJ databases.

EMBL; AL844509; CAD52286.1; -.

Hypothetical protein.

SEQUENCE 2518 AA; 304135 MW; 8953AF19D54B7789 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                  Gaps
                        Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oguchi K., Tamura K., Takahashi H.;
"Molecular cloning and characterization of OsTERT, a telomerase
reverse transcriptase homolog in Oryza sativa.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF288216; AAK35007.1; -.
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                                                                                                                                                                                          41.0%; Score 57; DB 2; Length 582; 58.8%; Pred. No. 2.7; 1ive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                         09A0EDBA03D96E23
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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InterPro, IPR001209; Ribosomal_S14.
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                                                                                                                                                       582 AA; 65720 MW;
                                                                                                                                                                                                                                                                                                   457 LPKPDNLRPILETAYVL 473
                                                                                                                                                                                                                                                                  11 IPKPDGLRPIVNMDYVV 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                           Local Similarity 58.8
nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=36329;
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                                                                                                                                                 SEQUENCE
                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C., Abrahameen M.S., "Telomerase reverse transcriptase gene and telomerase activity in Cryptosporidium parvum."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                   Lill SEQUENCE FROM N.A.

Kuramoto M., Ishikawa F.;

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

R EMBL; AF212299; AA643437.1; -.

R InterPro; IPR000477; RVTse.

R InterPro; IPR003545; Telomerase_RT.

Pfam; PR00178; TELOMERASERT.

R RINTS; PR01365; TELOMERASERT.

W RNA-directed DNA polymerase; Transferase.
                                                                                                                                                                                                                                                                                                                                      50.4%; Score 70; DB 13; Length 1191; 82.4%; Pred. No. 0.055;
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T 01-MAR-2003 (TrEMBLrel. 23, Created)
T 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
T 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
T 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Eptide synthetase (Fragment).
Fischerella sp. CENA19.
Bacteria; Cyanobacteria; Stigonematales; Fischerella.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cryptosporidium parvum.
Eukaryota, Alveolata, Apicomplexa, Coccidia, Eimeriida,
Cryptosporidiidae, Cryptosporidium.
NCBI_TaxID=5807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.2%; Score 60; DB 5; 45.0%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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INTERPPO, IRRN01064; Crystallin.
PROSTITE: PS00225; CRYSTALLIN BETAGAWMA; 1.
RNA-directed DNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        652 KIRWVPKSKGLRPLINLSKV 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Telomerase reverse transcriptase
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                                                                                                                                                                                                                                                                                                                                                                          1;
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Best Local Similarity 45.0°
Matches 9; Conservative
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Matches 14; Conservative
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                                                       Xenopodinae, Xenopus
NCBI_TaxID=8355;
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36.0%;
91.7%;
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Romero D.P., Ye A.J.;
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Best Local Similarity
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   SEQUENCE FROM N.A.
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Q9GRC5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group).
Wakaryota, Viridiplantes, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; Ehrhartoideae; Oryzeae, Oryza,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=cv. Nipponbare;
MEDLINE=22096152; PubMed=12100484;
Heller-Uszynska K., Schnippenkoetter W., Kilian A.;
"Cloning and characterization of rice (Oryza sativa L) telomerase reverse transcriptase, which reveals complex splicing patterns.";
Plant J. 11:75-86(2002).
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Sordariales, Sordariaceae, Neurospora.
NCBI_TaxID=5141;
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                                                                                                                                                                                                                           / Match 40.3%; Score 56; DB 10; Length 1259; Local Similarity 47.4%; Pred. No. 9; Indels 1; Indels 1; Indels 1; Mismatches 3; Mismatches 4; Mismatches 3; Mismatches 4; Mismatches
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InterPro; IPR003545; Telomerase_RT.
Pfam; PF00078; rvt; 2.
PRINTS; PR0135; TELOMERASERT.
PROSITE; PR00527; RIBOSOMAL S14; 1.
RNA-directed DNA polymerase; Transferase.
SEQUENCE 1261 AA; 143715 MW; 353153D1C8B7D5CB CRC64;
                           InterPro; IPR003545; Telomerase_RT.
Pfam; PF00078; rvt; 2.
PRINTS; PR01365; TELOMERASERT.
PROSITE; PS005125 PROSCOMB, S14; 1.
RNA-directed DNA polymerase; Transferase.
SEQUENCE 1259 AA; 143710 MW; 15B041789F2D5CAD CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Related to integral membrane protein PTH11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Telomerase reverse transcriptase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1261 AA
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InterPro; IPR001209; Ribosomal_S14.
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755 SSRVRFLPKAKDMRPLVDL 773
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InterPro; IPR000477; RVTse.
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Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
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STRAIN=KNZ-5 and KNZ-2;
MEDINE=21147925; PubMed=11250070;
Takenaka Y., Matsuura T., Haga N., Mitsui Y.;
"Expression of telomerase reverse transcriptase and telomere elongation during sexual maturation in Paramecium caudatum.";
Gene 264:153-161(2001).
                                                                                                                                                                                                                                                                                 Score 50; DB 3; Length 355;
Pred. No. 19;
0; Mismatches 1; Indels
Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., I
Nyakatura G., Mewes H.W., Mannhaupt G.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 895;
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                                                                                                                                              German Neurospora genome project;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL807366; CAD3567.1; -
SEQUENCE 355 AA; 39446 MW; 10EF0466F9F3B761 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AB0353109; BAB18587.1; -.
InterPrc; IPR00047; RVTse.
InterPrc; IPR003545; Telomerase_RT.
Pfam; PF00078; rvt; 2.
PRINTS; PR01365; TELOMERASERT.
RNA-directed DNA polymerase; Transferase.
SEQUENCE 895 AA; 107086 MW; 130C0DB32FD11C76 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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EMBL, AJ236415; CAB96263.1; -.
InterPro; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
Transmembrane.
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                                                                                                                                                                                                                                  0; Gaps
"A unique pause pattern during telomere addition by the error-prone telomerase from the ciliate Paramecium tetraurelia.";
Gene 0:0-0 (2002).
EMBL, AF515460; AAN03860.1; -.
InterPro; IPR003545; Telomerase_RT.
InterPro; IPR003545; Telomerase_RT.
Ffam, PR000709; rvt. 2.
PRINTS; PR01365; TELOMERASERT.
RNA-directed DNA polymerase; Transferase.
SEQUENCE 896 AA; 107237 MW; 697031F9DD61A883 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roques P., Robertson D., Sandrine S., Christel D., Francois S., Philippe M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 35.3%; Score 49; DB 15; Length 216; Best Local Similarity 50.0%; Pred. No. 16; Matches 9; Conservative 2; Mismatches 7; Indels
                                                                                                                                                                                          Query Match

36.0%; Score 50; DB 5; Length 896;
Best Local Similarity 60.0%; Pred. No. 54;
Matches 9; Conservative 2; Mismatches 4; Indels
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NON_TER 216 216
SEQUENCE 216 AA; 25003 MW; 0A5AC218BFA88932 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus 1.
Viruses, Retroid viruses; Retroviridae, Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Gp41 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                       216 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=YBF26
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Search completed: November 12, 2003, 19:50:46 Job time : 25.978 secs

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Truncated telomera Human telomerase p Altered C-terminus Altered C-terminus

us-08-854-050-115.rag

Sequence:

Run on:

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Database

Result No.

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Altered C-terminus
Altered C-terminus
Telomerase protein
Telomerase (ver. 2
Human telomerase r
                                                                                                                                                                                                                                                                                                                                   Human protein #2.
Heart muscle cell
Human telomerase r
Human telomerase r
Human telomerase p
Telomerase g
Glutathione-S-tran
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Truncated telomera
Truncated telomera
Truncated telomera
N-terminal truncat
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prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human telomerase reverse transcriptase antigenic peptide A-1.
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                                             AAY00651
AAY00639
AAY00648
AAW61349
AAY00643
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AAY00649
AAY00641
AAY00650
AAW71376
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AAY00638
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AABB2765
AAB99930
AAG64329
AAG64859
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AAY32090
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AAY26580
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ABP56676
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97US-0844419.
97US-0846017.
97US-0851843.
97US-0911312.
97US-0912951.
 97GB-0020890
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(GERO-) GERON CORP
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18-APR-1997;
25-APR-1997;
06-MAY-1997;
09-MAY-1997;
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 HTERT fragment with Amino acid sequence Human CRT-1 protein N-terminal truncat N-terminal truncat A catalytic telome Human CRT-1 protein Human CRT-1 protein
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                                                                            2003, 19:41:04 ; Search time 34.8679 Seconds (without alignments) 127.462 Million cell updates/sec
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1982.DAT:*
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                                                                                                                                                                                                                                      1107863
        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                   1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
                                                                                                                                                                                                              1107863 segs, 158726573 residues
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                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                      OM protein - protein search, using sw model
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AAW97385
AAY25461
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AAY00635
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AAY00634
AAY25463
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Maximum DB seq length: 200000000
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11446
11446
11466
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Moller

Gaudernack G,

Eriksen JA,

Lingner J;

(GEMV-) GEMVAX AS.

WPI; 2002-750459/81.

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The present sequence represents an antigenic peptide from human telomerase reverse transcriptase (HTRT), from the present invention. The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polymucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein preparation of recombinant telomerase by contacting a protein preparation of recombinant telomerase by contacting a protein preparation of the hTRT NNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of NNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of hTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTRT expression; and (B) the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibiting ageing . A protein preparation of hTRT and the polymucleotide encoding hTRT can be used in the manufacture of medicaments for inhibiting the profuse of ageing or cancer. Inhibitors of telomerase activity can be effect of ageing or cancer. Inhibitors of telomerase activity can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; telomerase catalytic subunit; hTERT; human leukocyte antigen; human telomerase reverse transcriptase; HLA epitope; cancer; HLA profile; breast cancer; pancreatic cancer; colorectal cancer; lung cancer; ovarian cancer; cervical cancer; malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma; anti-cancer; mutant; cytostatic; HLA class I epitope; HLA class II epitope; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activity. A protein preparation of hTRT can also be used in the new
                                                                                                                                                    Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treat conditions that are associated with high telomerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 146; DB 19;
100.0%; Pred. No. 5.1e-14;
ive 0; Mismatches 0;
                                             Harley C,
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                                             Chapman KB,
Harley CB;
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                                                                                                                                                                                                                                             Example 8; Fig 54; 387pp; English.
(UYTE-) UNIV TECHNOLOGY CORP
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                                           , Cech TR,
Nakamura T,
                                                                                                             WPI; 1998-171633/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 28; Conserv
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                                                                  Morin GB,
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The present invention relates to a polypeptide comprising a 20 amino acid sequence derived from human telomerase catalytic subunit con human telomerase reverse transcriptase, hTERT) amino acid sequence for human telomerase reverse transcriptase, hTERT) amino acid sand at least two human leukocyte antigen (HLA) class I or class II captopes. The invention also describes a polypeptide having the above contained and peptide sequence as additional C and/or N-terminal sequences on a fragment of hTERT which is not more than 100 amino acids of hTERT. The polypeptides of the invention are useful in a acids of hTERT composition or in a vaccine for preventing or treating cancer in populations of individuals having varying HLA profiles. The polypeptides of the invention are useful in a cancers such as breast, pancreatic, colorectal, lung, ovarian or cancers such as breast, pancreatic, colorectal, lung, ovarian or cervical cancer, malignant melanoma, leukaemia, lymphoma or biliary tract carcinoma. The polypeptides or encoding polymuclectide sequences are useful for performing identity, sequence homology and/or hybridisation studies, for predicting structure and/or function (e.g. anti-cancer activity), or for screening methods in the present a hTERT fragment with the 20 amino acid HLA epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New catalytic protein of telomerase of a higher animal and a gene coding it - useful for diagnosis of diseases caused by the change in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                 New polypeptide with an additional C-terminal and/or N-terminal sequence, useful for preparing anti-cancer vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    containing polypeptide at its N-terminus.
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                                                                                                                                                         Disclosure; Fig 1; 62pp; English.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel gene, useful in detection of telomerase activity and cancer cells as well as screening telomerase inhibitors for treatment of
                                                                                                                                                                                                                                                                                                   CRT-1; reverse transcriptase; telomerase; inhibitor; detection; telomerase activity; cancer cell; screening; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Partial sequence, no stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 438;
                         Indels
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100.0%; Pred. No. 8.4e-13;
tive 0; Mismatches 0;
                         ö
      Pred. No. 8.4e-13;
100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 AKFLHWLMSVYVVELLRSFFYVTETTFQ 59
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                                                                         32 AKFLHWLMSVYVVELLRSFFYVTETTFQ
                                                        1 AKFLHWLMSVYVVELLRSFFYVTETTFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 35-36; 44pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                       AAY25462 standard; Protein; 438
                                                                                                                                                                                                                                                                                                                                                                                                     1..438
/label= CRT-1
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98JP-0033584.
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                                                                                                                                                                                                                                    (first entry)
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      Best Local Similarity 100.
Matches 28, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tsuchiya M, Yoshida K;
                                                                                                                                                                                                                                                                     Human CRT-1 protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-430393/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     438 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAX88250
                                                                                                                                                                                                                                    22-SEP-1999
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9935261-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-1998;
                                                                                                                                                                                                    AAY25462;
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AAY00635
ID AAY0
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                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel human CRT-1 genes and their encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel gene, useful in detection of telomerase activity and cancer cells as well as screening telomerase inhibitors for treatment of
                                                               The specification describes a human catalytic telomerase protein. The products are useful in drug compositions for the diagnosis of diseases caused by the change in activity of telomerase. The present sequence appears in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRT-1; reverse transcriptase; telomerase; inhibitor; detection; telomerase activity; cancer cell; screening; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..437
/label= CRT-1
/note= "Partial sequence, no stop codon given"
                                                                                                                                                                                    Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 146; DB 20; Length 437;
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                                                                                                                                                                                 100.0%; Score 146; DB 20;
100.0%; Pred. No. 2.5e-13;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                  28
                                                                                                                                                                                                                                                                 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                  Example 1; Page 14; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                               AAY25461 standard; Protein; 437 AA
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98JP-0013232.
98JP-0033584.
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                                                                                                                                                                                                                28; Conservative
   of a telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yoshida K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human CRT-1 protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-430393/36.
                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                 131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    437 AA;
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08-JAN-1998;
30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                 AAY25461;
   activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
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                                                                                                                                                                                                                Matches
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AAY00635;

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This sequence is a truncated human telomerase of the invention. Primers that amplify the telomerase coding sequence can be used in a method for diagnosing cancer in a patient. The telomerase can be used to diagnosis and drug screening. Inhibitors of telomerase activity can be used to treat cancers such as melanomas, other skin cancers, neuroblastomas, breast carcinomas, colon carcinomas, cother skin growths. Enhancers of telomerase may be used to stimulate stem or skin growths. Enhancers of telomerase may be used to stimulate stem cell proliferation and differentiation (expansion of haematopoietic stem cells could be administered in the born marrow transplant context). As well, many tissues have stem cells. Proliferation of these cells may be useful in wound healing, hair growth, treatment of disease such as Wilm's tumour, organ regeneration or differentiation after injury or diseases, nerve cell or brain cell growth following injury.

Note: The N-terminus of this sequence can be replaced by the sequences shown in AAYO0656-Y00658.
                                         Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia; euroblastoma; breast carciinoma; colon carciinoma; orgeosarcoma; smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour; stem cell differentiation; organ regeneration; organ differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated vertebrate telomerase genes - used to develop products for treating cancers or for organ regeneration, nerve cell or brain cell growth following injury or bone marrow transplantation
N-terminal truncated telomerase (ver. 2) protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 146; DB 20;
100.0%; Pred. No. 1.1e-12;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKFLHWLMSVYVVBLLRSFFYVTETTFQ 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Fig 11t-u; 134pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CAMB-) CAMBIA BIOSYSTEMS LLC.
                                                                                                                                                                                                                                                                                                                                                          97US-0058287.
97US-0051410.
97US-0053018.
97US-0053329.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAX18272.
                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1997;
21-JUL-1997;
21-JUL-1997;
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                                                                                                                                                                                                                          WO9901560-A1.
                                                                                                                                                              sapiens
                                                                                                                                                                                                                                                                                                                01-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                            09-SEP-1997;
                                                                                                                                                                                                                                                                      14-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bowtell D,
                                                                                                                                                                              Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is a truncated human telomerase of the invention. Primers that amplify the telomerase coding sequence can be used in a method for diagnosing cancer in a patient. The telomerase can be used for detection, diagnosis and drug screening. Inhibitors of telomerase activity can be used to treat cancers such as melanomas, other skin cancers, neuroblastomas, breast carcinomas, colon carcinomas, lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin growths. Enhancers of telomerase may be used to stimulate stem cells proliferation and differentiation (expansion of haematopoietic stem cells could be administered in the bone marrow transplant context). As
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      well, many tissues have stem cells. Proliferation of these cells may be useful in wound healing, hair growth, treatment of disease such as Wilm's tumour, organ regeneration or differentiation after injury or diseases, nerve cell or brain cell growth following injury.
                                                                                                                                    Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia; neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma; smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour; stem cell differentiation; organ regeneration; organ differentiation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated vertebrate telomerase genes - used to develop products for treating cancers or for organ regeneration, nerve cell or brain cell growth following injury or bone marrow transplantation
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                                                                                          N-terminal truncated telomerase protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CAMB-) CAMBIA BIOSYSTEMS LLC.
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97US-0051410.
97US-0053018.
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                                                (first entry)
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N-PSDB; AAX18263.
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Best Local Similarity
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                                                                                                                                                                                                                                                      sapiens
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                                              26-JUL-1999
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21-JUL-1997

Synthetic.

Ношо

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Gaps

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Indels

A catalytic telomerase protein.

(first entry)

26-JUL-1999

AAY00644;

RESULT 7 AAY00644

g ð

Matches

Length 588;

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The present sequence represents a human telomerase reverse transcriptase
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                          This invention describes novel human CRT-1 genes and their encoded proteins containing a reverse transcriptase motif, which act as telomerase inhibitors. The gene, its encoded protein and derived antibodies can be used to provide base sequence information, detect telomerase activity and cancer cells, and to screen telomerase inhibitors. The detection method is simple and effective.
                                 Novel gene, useful in detection of telomerase activity and cancer cells as well as screening telomerase inhibitors for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
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                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reverse transcriptase; hTRT; TRT; diagnosis;
                                                                                                                                                                                                                                                                    Length 622;
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                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human telomerase reverse transcriptase Delta182 variant.
                                                                                                                                                                                                                                                                    / Match 100.0%; Score 146; DB 20; Local Similarity 100.0%; Pred. No. 1.2e-12; Nes 28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                             59
                                                                                                                                                                                                                                                                                                                                 1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
                                                                                                                                                                                                                                                                                                                                                32 AKFLHWLMSVYVVELLRSFFYVTETTFQ
                                                                                              Example 1; Page 37-39; 44pp; Japanese
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Harley CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW46997 standard; Protein; 807 AA
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97US-0844419.
97US-0846017.
97US-0851843.
97US-0854050.
97US-0911312.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-171633/16.
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                                                                                                                                                                                                                                     622 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; telomerase
    N-PSDB; AAX88251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAV22382.
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18-APR-1997
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06-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                    Query Match
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                                                                     cancers
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                                                                                                                                                                                                                                                              New catalytic protein of telomerase of a higher animal and a gene coding it - useful for diagnosis of diseases caused by the change in activity of a telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a catalytic telomerase protein. The products are useful in drug compositions for the diagnosis of diseases caused by the change in activity of telomerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     telomerase; inhibitor; detection;
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/label= CRT-1
/note= "Partial sequence, no stop codon given"
Catalytic telomerase; diagnosis; disease; telomerase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 591;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   telomerase activity; cancer cell; screening; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 146; DB 20; ilarity 100.0%; Pred. No. 1.1e-12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 11-14; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY25463 standard; Protein; 622 AA
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                                                                                                                                                                                    (MITU ) MITSUBISHI CHEM CORP
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98JP-0013232.
98JP-0033584.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fsuchiya M, Yoshida K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human CRT-1 protein #3
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N-PSDB; AAX15923.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      591 AA;
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08-JAN-1998;
30-JAN-1998;
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                              Homo sapiens
                                                           JP11046768-A
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Protein
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describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein of preparation of hTRT with a telomerase RNA component; (C) detection of the hTRT with a telomerase RNA component; (C) detection of the hTRT with a telomerase RNA component; (C) detection of the hTRT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of intro a sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTRT expression; and (B) the use of an agent that causes an increase in cell correlation proparation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polynucleotide encoding hTRT can be used in the manufacture of medicaments for inhibiting the used to treat conditions that are associated with high telomerase used in the new activity. A protein preparation of hTRT can also be used in the new
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100.0%; Pred. No. 1.6e-12;
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97US-0051410.
97US-0053018.
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97US-0054642.
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Matches 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         807 AA;
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Claim 4; Fig 11d-e; 134pp; English

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          This sequence is a truncated human telomerase of the invention. Primers that amplify the telomerase coding sequence can be used in a method for diagnosing cancer in a patient. The telomerase can be used for detection, diagnosing cancer accenting. Inhibitors of telomerase activity can be used to treat cancers such as melanomas, other skin cancers, neuroblastomas, breast carcinomas, colon carcinomas, leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin growths. Enhancers of telomerase may be used to stimulate stem cell proliferation and differentiation (expansion of haematopoietic stem cells could be administered in the bone marrow transplant context). As well, many tissues have stem cells. Proliferation of these cells may be tumour, organ regeneration or differentiation after injury or diseases, nerve cell or brain cell growth following injury.
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100.0%; Pred. No. 1.6e-12;
ive 0; Mismatches 0;
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97US-0053018.
97US-0053329.
97US-0054642.
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                                                                                                                                                                                                                                                                                807 AA;
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21-JUL-1997;
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Bowtell D, Kilian A;
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21-JUL-1997;
21-JUL-1997;
04-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma; smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour; stem cell differentiation; organ regeneration; organ differentiation.
be used for detection, diagnosis and drug screening. Inhibitors of telomerase activity can be used to treat cancers such as melanomas, other skin cancers, neuroblastomas, breast carcinomas, colon carcinomas, leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin growths. Enhancers of telomerase may be used to stimulate stem cell proliferation and differentiation (expansion of haematopoietic stem well, many tissues have stem cells. Proliferation of these cells may be well, many tissues have stem cells. Proliferation of these cells may be wilm's tumour, organ regeneration or differentiation after injury or diseases. nerve cell or brain cell growth following injury. Note: The Niterminus of this sequence can be replaced by the sequences
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                                                                                                                                                                                               Length 807;
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97US-0053018.
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Best Local Similarity 100...
...hes 28; Conservative
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21-JUL-1997
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                                                                                                                                             cells could be administered in the bone marrow transplant context). As well, many tissues have stem cells. Proliferation of these cells may be useful in wound healing, hair growth, treatment of disease such as Wilm's tumour, organ regeneration or differentiation after injury or diseases, nerve cell or brain cell growth following injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma; smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour; stem cell differentiation; organ regeneration; organ differentiation.
                                    leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin growths. Enhancers of telomerase may be used to stimulate stem cell proliferation and differentiation (expansion of haematopoietic stem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Telomerase, human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated vertebrate telomerase genes - used to develop products for treating cancers or for organ regeneration, nerve cell or brain cell growth following injury or bone marrow transplantation
skin cancers, neuroblastomas, breast carcinomas, colon carcinomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Truncated telomerase (ver. 2) protein sequence lacking motif A.
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100.0%; Pred. No. 1.6
ive 0; Mismatches
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28; Conservative C
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97US-0053018.
97US-0053329.
97US-0054642.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia; neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma; smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour; stem cell differentiation; organ regeneration; organ differentiation.
cells could be administered in the bone marrow transplant context). As well, many tissues have stem cells. Proliferation of these cells may be useful in wound healing, hair growth, treatment of disease such as Wilm's tumour, organ regeneration or differentiation after injury or diseases, nerve cell or brain cell growth following injury. Note: The N-terminus of this sequence can be replaced by the sequences
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated vertebrate telomerase genes - used to develop products for treating cancers or for organ regeneration, nerve cell or brain cell growth following injury or bone marrow transplantation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-terminal truncated telomerase protein sequence.
                                                                                                                                                                                                                                                                                           542 AKFLHWLMSVYVVELLRSFFYVTETTFQ 569
                                                                                                                                                                                                                                                        1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
                                                                                                                                                                                                                                                                                                                                                                                  AAY00639 standard; Protein; 948 AA
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97US-0053018.
97US-0053329.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                           shown in AAY00656-Y00658.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-106060/09.
                                                                                                                                                936 AA;
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21-JUL-1997
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04-AUG-1997
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                                                                                                                                                  Sequence
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useful in wound healing, hair growth, treatment of disease such as Wilm's tumour, organ regeneration or differentiation after injury or diseases, nerve cell or brain cell growth following injury.
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100.0%; Pred. No. 1.8e-12;
ive 0; Mismatches 0;
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us-08-854-050-115.rpr

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

2003, 19:43:04 ; Search time 10.9182 Seconds (without alignments) 246.626 Million cell updates/sec November 12, Run on:

US-08-854-050-115 146 1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_76:* 1: pir1:* 3: pir2:* pir3:* pir4:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Description | telomerase catalvt | | | telomerase catalyt | U | | cationic amino aci | cationic amino aci | telomerase reverse | probable benzoate | hypothetical prote | protein F56E10.3 [| probable copper tr | T | conserved hypothet | | hypothetical 18.7K | | hydrogenase (EC 1. | • | heat shock protein | hetical | oligopeptide ABC t | hypothetical prote | 4 | hypothetical prote | interferon beta-1 | G protein-coupled | NADH2 dehydrogenas |
|-----------|---------------|--------------------|-----|--------|--------------------|--------|--------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------|--------------------|-----------------|--------------------|--------|--------------------|--------|--------------------|---------|--------------------|--------------------|--------|--------------------|-------------------|-------------------|--------------------|
| SUMMAKIES | | T03844 | ~ | A49518 | 853396 | T41134 | B97775 | C97751 | F71686 | T31107 | B71543 | T30621 | F88921 | T39949 | D97248 | E75436 | E64112 | S21858 | D58933 | A64599 | D71915 | C69175 | AC3102 | G98184 | E72305 | S67794 | A85139 | IVHUB1 | T44011 | S52967 |
| | DB | . 7 | 7 | 7 | 7 | 7 | ~ | ~ | ~ | ~ | 7 | ~ | ~ | ~ | 7 | ~ | , -1 | ~ | 7 | - | 7 | - | ~ | 7 | 7 | ~ | 0 | Н | 7 | 7 |
| | Length | 1132 | 989 | 427 | 884 | 521 | 102 | 465 | 470 | 1132 | 302 | 663 | 200 | 148 | 231 | 340 | 398 | 163 | 267 | 224 | 224 | 258 | 316 | 316 | 835 | 1125 | 456 | 187 | 301 | 554 |
| de | ery | 100.0 | വ | 37.0 | 37.0 | è. | ς. | S. | 4 | 34.9 | • | 4. | 34.2 | | 'n | 'n. | 'n. | 32.5 | ς. | ď | | | | • | | • | • | | | |
| | Score | 146 | 81 | 54 | 54 | 53.5 | 52 | 25 | 51 | LO. | 50.5 | 50.5 | 20 | 49 | 48 | 48 | 48 | 47.5 | 47.5 | 47 | 47 | 47 | 47 | 47 | 47 | 47 | 46.5 | | 46 | 46 |
| | Result No. | | 8 | æ | 4 | S | 9 | 7 | æ | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | | 28 | |

| NADH2 dehydrogenas | protein T32E20.25 | probable fimbrin [| hypothetical prote | hypothetical prote | hypothetical prote | hypothetical prote | prolipoprotein dia | sugar ABC transpor | hypothetical prote | hypothetical prote | cytochrome-c oxida | NADH2 dehydrogenas | conserved hypothet | hypothetical prote | ycf9 protein - Chl |
|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| S07744 | B86489 | A84461 | F70578 | S39340 | H86713 | A86670 | F71712 | G72357 | 842371 | G64492 | 875109 | T13682 | D70128 | T04979 | T08028 |
| 7 | 0 | ~ | 0 | ~ | ~ | ~ | ~ | ~ | ~ | ~ | ~ | 7 | 7 | ~ | ~ |
| 570 | 371 | 652 | 96 | 120 | 203 | 214 | 268 | 277 | 405 | 441 | 544 | 744 | 971 | 710 | 62 |
| 31.5 | 31.2 | 31.2 | 30.8 | 30.8 | 30.8 | 30.8 | 30.8 | 30.8 | 30.8 | 30.8 | 30.8 | 30.8 | 30.8 | 30.5 | 30.1 |
| 46 | 45.5 | 45.5 | 45 | 45 | 45 | 45 | 45 | 45 | 45 | 45 | 45 | 45 | 45 | 44.5 | 44 |
| 0 | _ | 2 | E | 34 | 35 | . 96 | 37 | 38 | 6 | 9 | 11 | 7 | 23 | 44 | 5 |

ALIGNMENTS

T03844

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NyAlternate names: telomerase reverse transcriptase
C;Species: Homo aspiens (man)
C;Decies: 1999 asequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C;Accession: T03844
S;Anakamura, T.M.; Morth, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J. A;Tile: Telomerase catalytic subunit homologs from fission yeast and human.
A;Reference number: 215111; MUID:97400623; PMID:9252327
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-1132 «NAK»
A,Essidues: 1-1132 «NAK»
A,Cross-references: EMBL.AP015950; NID:g2330016; PIDN:AAC51672.1; PID:g2330017
A,Experimental source: kidney
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A;Gene: TRT
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Matches
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NAILernate names: telomerase reverse transcriptase 1 C;Species: Schizosaccharomyces pombe C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 01-Dec-2000 C;Accession: T03838; T03839; T40085 Schence 277, 955-959, 1997 A;Title: Telomerase catalytic subunit homologs from fission yeast and human. A;Reference number: 215111; MUID:97400623; PMID:9252327 A;Accession: T03838 telomerase catalytic chain - fission yeast (Schizosaccharomyces pombe)

A;Residues: 1-989 cNAK> A;Cross-references: EMBL:AF015783; NID:g2340167; PIDN:AAC49803.1; PID:g2340169 A;Experimental source: strain 972h(-)

A;Accession: T03839
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Nolecule type: DNA
A;Residues: 1-524,526-989 <NA2>
A;Cross-references: EMBL:AF015783; NID:g2340167; PIDN:AAC49802.1; PID:g2340168

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A;Molecule type: DNA
A;Residues: 1-884 cDUZ.
A;Cross-references: EMBL:U20618; NID:92258165; PID:9662136; GSPDB:GN00012; MIPS:YLR318w
A;Experimental source: strain S288C (AB972)
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C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
C;Accession: B97775
R;Ogata, H; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R
Science 293, 2093-2098, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-521 <LYN>
A;Cross-references: EMBL:AL022598; PIDN:CAA18644.1; GSPDB:GN00068; SPDB:SPCC1795.09
A;Experimental source: strain 972h-; cosmid c1795
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                                                                                                                                                                                                                                            telomerase catalytic chain EST2 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein L8543.12; protein YLR318w
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 05-Nov-1999
C;Accession: S53396
R;Du, Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aspartic acid proteinase - fission yeast (Schizosaccharomyces pombe)
C,Species: Schizosaccharomyces pombe
C,Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Oliver, K.; Harris, D. submitted to the EMBL Data Library, April 1998
A;Reference number: Z21971
A;Accession: T41134
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: D.V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, February 1995
A,Description: The sequence of S. cerevisiae cosmid 8543.
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36.6%; Score 53.5; DB 2;
Best Local Similarity 34.4%; Pred. No. 4.5;
Matches 11; Conservative 7; Mismatches 9;
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6.3;
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Pred, No. 6.3;
7; Mismatches
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A;Gene: SGD:EST2, MIPS:YLR318w
Z;Cross-references: SGD:S0004310; MIPS:YLR318w
A;Map position: 12R
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Best Local Similarity 36.4%;
Matches 8; Conservative
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A, Map position: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S53396
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-427 - cCH2.
A;Cross-references: 1-427 - cCH2.
B;Zhou, G.X.; Chao, L.; Chao, J.
J. Biol. Chem. 267, 25873-25880, 1992
A;Title: Kallistatin: a novel human tissue kallikrein inhibitor. Purification, character
A;Reference number: A45093; MUID:93100304; PMID:1334488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Molecule type: mRNÅ

*Residues: 1-427 - CCHA-

A, Cross-references: GB:L19684; NID:g425145; PIDN:AAA59454.1; PID:g425146

A;Cross-references: GB:L19684; NID:g425145; PIDN:AAA59454.1; PID:g425146

R;Chal, K.X.; Ward, D.C.; Chao, J.; Chao, L.

Genomics 23, 370-378, 1994

A;Title: Molecular cloning, sequence analysis, and chromosomal localization of the human

A;Reference number: A55560; MUID:95137583; PMID:7835886
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A;Map position: 14q31-14q32.1
C;Superfamily: antithrombin III
C;Superfamily: antithrombin III
C;Superfamily: antithrombin III
C;Keywords: blocked amino end; glycoprotein; pyroglutamic acid; serine proteinase inhibi
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-427/Product: kallistatin #status predicted <MAT>
F;21/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;33,108,157,238/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;388/Inhibitory site: Phe (tissue kallikrein) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kallistatin precursor - human
NyAlternate names: proteinase inhibitor 4; tissue kallikrein inhibitor
NyAlternate names: proteinase inhibitor 4; tissue kallikrein inhibitor
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A49518; A55560; A45093
R;Chai, K.X.; Chen, L.M.; Chao, J.; Chao, L.
J. Biol. Chem. 268; 24498-24505, 1993
A;Title: Kallistatin: a novel human serine proteinase inhibitor. Molecular cloning, tiss
A;Reference number: A49518; MUID:94043294; PMID:8227002
                                                                                                                                                                                                                                                                                                                                                  A,Map position: 2
A;Introns: 86/3; 113/3; 153/2; 241/1; 372/1; 395/3; 485/3; 524/3; 582/2; 644/1; 693/3;
C;Keywords: alternative splicing
                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-524,526-989 <LYN>
A;Residues: 1-524,526-989 <LYN>
A;Cross-references: EMBL:AL022299; PIDN:CAA18391.1; GSPDB:GN00067; SPDB:SPBC29A3.14c
A;Experimental source: strain 972h-; cosmid c29A3
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Pred. No. 3.2;
4; Mismatches 11; Indels
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A;Cross-references: PIDN:AAB24557.1; PID:g261993
A;Note: sequence extracted from NCBI backbone (NCBIP:120847)
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.
submitted to the EMBL Data Library, March 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.5%; Score 81; DB 2; L 42.3%; Pred. No. 0.00079; iive 12; Mismatches 3;
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46.4%;
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Matches 11, Conservative
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Best Local Similarity 46.4
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                     A; Gene: trt1; SPBC29A3.14c
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C.Species: Oxytricha trifallax
C.Species: Oxytricha trifallax
C.Species: Oxytricha trifallax
C.Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C.Accession: T3107
R.Bryan, T.M.; Specger, J.M.; Chapman, K.B.; Cech, T.R.
Proc. Natl. Acad. Sci. U.S.A. 95, 8479-8484, 1998
A.Title: Telomerase reverse transcriptase genes in Tetrahymena thermophila and Oxytrich A.Feference number: 220985; MUID:98337940; PMID:9671703
A.Accession: T31107
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-1132 -BRY>
A.Conserreferences: EMBL:AF060230; NID:93342795; PID:93342796; PIDN:AAC39163.1
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C, Species: Chlamydia trachomatis
C, Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 20-Apr-2000
C, Accession: B71543
R; Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell
Science 282, 754-759, 1998
A; Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra
A; Reference number: A71570; MUID:99000809; PMID:9784136
A; Accession: B71543
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: LNA
A; Molecule t
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NyAlternate names: Mol9L
C;Species: Molluscum contagiosum virus 1
C;Species: Molluscum contagiosum virus 1
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-May-2000
C;Accession: T30621
S;Sankevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
S;Cience 273, 813-816, 1996
A;Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host r
A;Reference number: 220876; MUID:96325459; PMID:8670425
A;Accession: T30621
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Pred. No. 22;
4; Mismatches 10; Indels
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A;Gene: ubiA
C;Superfamily: 4-hydroxybenzoate octaprenyltransferase
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             448 IYWFITIFILYLVRSFF 464
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Local Similarity 39.1%;
es 9; Conservative '
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Local Similarity 40.9%;
les 9; Conservative
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Cipactes 21.Nov-1998 #sequence_revision 21.Nov-1998 #text_change 03.Nov-2000
CiAccession: F71686
Shadersson, S.G.B.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U Nature 396, 133-140, 1998
A; Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A; Reference number: A71630; MUID:99039499; PMID:9823893
A; Accession: F71686
A; Reference number: A70630; MUID:99039499; PMID:9823893
A; Residues preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-470 cANDA
A; Residues: 1-470 cANDA
A; Cross-references: GBAA235271; GB:AJ235269; NID:93868717; PIDN:CAA14768.1; PID:9386086
A; Experimental source: strain Madrid E
C; Genetics:
A; Gen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Rickettsia conorii (strain Ma C.Species: Rickettsia conorii (strain Ma C.Species: Rickettsia conorii (strain Ma C.Species: Rickettsia conorii (Spate: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 17-May-2002 C;Accession: C97751 R:Ggata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, I A:Ritle: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893 A;Accession: C97751 A;Status: preliminary A;Nolecule type: DNA A;Nolecule type: DNA A;Residues: 1-465 <KUR>
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
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                                                                                A; Accession: B97775
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-102 < KUR>
A; Cross-references: GB: AE006914; PIDN: AAL03140.1; PID: g15619686; GSPDB: GN00173
A; Genetics:
A; Genetics:
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A;Gene: atrCl
C;Superfamily: arginine permease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
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Pred. No. 1.6;
4; Mismatches
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Best Local Similarity 33.3%; Pred. No. Matches 7; Conservative 9; Mismatc
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Best Local Similarity 50.01
Matches 8; Conservative
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Best Local Similarity
Matches 6; Conserv
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Conserved membrane protein, YccA family [imported] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C; Accession: D97248 R; Accession: D97248 R; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. Barcan, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Accession: E75436
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.; Shen, M.; Vener, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
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A;Cross-references: GB:AE001961; GB:AE000513; NID:g6458843; PIDN:AAF10688.1; PID:g64588
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: GB:AE001437, PIDN:AAK80775.1, PID:g15025874, GSPDB:GN00168
A,Experimental source: Clostridium acetobutylicum ATCC824
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Pred. No. 19;
3; Mismatches
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50.0%;
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Best Local Similarity 50.0
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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A; Residues: 1-231 < KUR>
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A; Status: preliminary
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A,Map position: 1
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A;Gene: CAC2831
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A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: F88921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB:chr_V; PIDN: AAC69222.1; PID: 93806156; GSPDB: GN00023; CESP: F56E10.
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A,Experimental source: strain 972h-; cosmid c23G7
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein F56E10.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
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                                                                                                                                         DB 2; Length 663;
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R;Xiang, Z.; Aves, S.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitred to the EMBL Data Library, January 1999
A;Reference number: Z21893
A;Accession: T39949
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14;
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A,Molecule type: DNA
A,Residues: 1-148 <XIA>
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                                                                                                                                         Score 50.5; DB
Pred. No. 16;
6; Mismatches
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Pred. No. 6.3;
7; Mismatches
A;Cross-references: EMBL:U60315; PIDN:AAC55147.1
C;Genetics:
A;Note: MC019L
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Pred. No. 14;
6; Mismatches
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A;Introns: 15/3; 24/2; 111/2; 118/3
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Best Local Similarity 40.6%;
Matches 13; Conservative 7
                                                                                                                                         34.6%;
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34.6%;
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Best Local Similarity 31.09
Matches 13; Conservative
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Best Local Similarity 34.61
Matches 9; Conservative
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Residues: 1-500 <STO>
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Gene: F56E10.3
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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A Londono-Vallejo J.A.;

I "Sequence of a BAC carrying the entire hTERT gene.";

"Sequence of a BAC carrying the entire hTERT gene.";

"Sequence of a BAC carrying the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR THE REPLICATION OF CHROMOSOME TERMINI IN MOST BURARYOTES. IT ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS SIMPLE SEQUENCE MITHIN THE RNA COMPONENT OF THE ENZYME.

-!- SUBGINIT: Interacts with PINXI.

-!- SUBCELLULAR LOCATION: NUCLear.

-!- DISEASE: ACTIVATION OF TELOMERASE HAS BEEN IMPLICATED IN CELL IMMORTALIZATION AND CANCER CELL PATHOGENESIS.

-!- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakamura T.M., Morin G.B., Chapman K.B., Weinrich S.L., Andrews W.H., Lingner J., Harley C.B., Cech T.R.; "Telomerase catalytic subunit homologs from fission yeast and human."; Science 277:955-959(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=97433088; PubMed=9288757;
Meyerson M., Counter C.M., Eaton E.N., Ellisen L.W., Steiner P.,
Caddle S.D., Ziaugra L., Beijersbergen R.L., Davidoff M.J., Liu Q.,
Bacchetti S., Haber D.A., Weinberg R.A.;
"HEST2, the putative human telomerase catalytic subunit gene, is upregulated in tumor cells and during immortalization.";
                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                   FUCK_ECOLI
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MEDLINE=97400623; PubMed=9252327;
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014746; 014783;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seqn
28-FEB-2003 (Rel. 41, Last ann
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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GO; GO:0003721; F:telomeric template RNA reverse transcriptas. . .; TAS.
GO; GO:0003721; F:telomere binding; TAS.
InterPro; IPR000477; RVTse.
InterPro; IPR003545; Telomerase_RT.
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Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL
THE REPLICATION OF CHROMOSOME TERMINI IN MOST BUTARYOTES. IT
ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS
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MEDLINE=98393668; PubMed=9724727;
Martin-Rivera L., Herrera E., Albar J.P., Blasco M.A.;
"Expression of mouse telomerase catalytic subunit in embryos and
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6.3e-14;
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1132 AA; 126996 MW; 94E35469C4CA33A0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 95:10471-10476 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Telomerase reverse transcriptase (EC 2.7.7.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1122 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         542 AKFLHWLMSVYVVELLRSFFYVTETTFQ 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 146; 100.0%; Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKFLHWLMSVYVVELLRSFFYVTETTFQ 28
                                                                                                                                              EMBL, AF015950; AAC51672.1; --
EMBL, AF128994; AAD3037.1; --
EMBL, AF128893; AAD30037.1; --
EMBL, AX007685; AAG23289.1; --
EMBL, AX03844; --
Genew; HGNC:11730; TERT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 550-616 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oncogene 16:1723-1730(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.0
Matches 28, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adult tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TERT_MOUSE S
070372; 035432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA-binding,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subunit).
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Nakamura T.M., Morin G.B., Chapman K.B., Weinrich S.L., Andrews W.H., Lingner J., Harley C.B., Cech T.R.;
"Ingner J., Harley C.B., Cech T.R.;
"Telomerase catalytic subunit homologs from fission yeast and human.";
Science 277:955-959(1997).
SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
SUBUNIT: Interacts with PINX1 (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
TELOMERASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TERT_SCHPO STANDARD; FK1; Journ.
013339; 01338;
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-1848401; PubMed=11859360; MEDLINE-1848401; PubMed=11859360; MEDLINE-21848401; PubMed=11859360; Med V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles M., Goble A., Harris D., Hidalgo J., Hodgson G., Holroyd S., Horneby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mingall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 78.8%; Score 115; DB 1; Length 1122; Local Similarity 75.0%; Pred. No. 2.6e-09; hes 21; Conservative 3; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 I -> V (IN REF. 3).
127977 MW; F85266905DD6558C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRT1 OR SPBC29A3.14C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  532 ATFLFWLMDTYVVQLLRSFFYITESTFQ 559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF073311; AAC34821.1; -.
EMBL; AF022235; AAB84200.1; -.
MGD; MGI:1202709; Tert.
InterPro; IPR000477; RVTse.
InterPro; IPR03545; Telomerase_RT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF051911; AAC09323.1; -.
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subunit) (Telomerase subunit P123).
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                                                                                               SEQUENCE FROM N.A.
                                                                    NCBI_TaxID=5940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
          8
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Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
A Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Bebel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
Bertym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Ber P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
Aucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
Daga R.R., Cruzado L., Moreno S., Armstrong J., Forsburg S.L.,
Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
T. The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                            ISOIG=013339-2; Sequence=VSP 006395; MISCELLANEOUS: DELETION CAUSES_TELOMERE SHORTENING AND SENESCENCE. SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
                                                                                                                                                                                                                                           NATURE 415:871-880 (2002).
-!- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein; DNA-binding; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ,
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            988 AA; 116328 MW; AB2DC7030228F443 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                006395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=013339-1; Sequence=Displayed;
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AEFIYWLYNSFIIPILQSFFYITESS 450
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                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Nuclear. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro, IPR000477; RVTse.
InterPro, IPR003545; Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GeneDB SPombe; SPBC29A3.14c; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF015783; AAC49803.1; -. EMBL; AL022299; CAA18391.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF015783; AAC49802.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELOMERASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR, T03838, T03838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00078; rvt;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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000939;
30-MAY-2000 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                   Name=1
                                                                                                                                                                                                                                                                                                                                                                                                                 Name=2
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Matches
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                                                                                                                                                                                                                                                                                                                          telomerase.";
Science 276:561-567(1997).
Science 276:561-567(1997).

THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT
THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT
ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS
SIMPLE SEQUENCE REPEATS TO CHROMOSOME BNDS BY COPYING A TEMPLATE
SEQUENCE WITHIN THE RAN COMPONENT OF THE ENZYME.

SUBCELLULAR LOCATION: Nuclear.

SUBCELLULAR LOCATION: THE REVERSE TRANSCRIPTASE FAMILY.

TELOMERASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR01365; TELOMERASERT.
Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-95137583; PubMed=7835886;
Chai K.X., Ward D.C., Chao J., Chao L.;
"Molecular cloning, sequence analysis, and chromosomal localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-SEP-2003 (Rel. 42, Last annotation update)
Kallistatin precursor (Kallikrein inhibitor) (Protease inhibitor 4)
SERPINA4 OR P14 OR KST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chai K.X., Chen L.-M., Chao J., Chao L.;
"Kallistatin: a novel human serine proteinase inhibitor. Molecular.
"Coloning, tissue distribution, and expression in Escherichia coli.";
J. Biol. Chem. 268:24498-24505(1993).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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`
Eukaryota, Alveolata, Ciliophora, Spirotrichea, Hypotrichia,
Euplotida, Euplotidae, Euplotes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.3%; Score 69; DB 1; Length 1031; 56.5%; Pred. No. 0.017;
                                                                                                                                                                                                                         Lingner J., Hughes T.R., Shevchenko A., Mann M., Lundblad
Cech T.R.;
                                                                                                                                                                                                                                                                                                   "Reverse transcriptase motifs in the catalytic subunit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1031 AA; 122562 MW; 57B87A63A1FED60F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           427 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.5%; Pred. No. 0.01
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 438 KLLRWIFEDLVVSLIRCFFYVTE 460
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InterPro; IPR003545; Telomerase_RT.
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MEDLINE=94043294; Pubmed=8227002;
                                                                                                                                                                                           MEDLINE=97274210; PubMed=9110970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P29622; 096B25;
01-APR-1993 (Rel. 25, Created)
01-OCT-1996 (Rel. 34, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U95964; AAC47515.1;
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es 13; Conservative
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                                                                                                                       A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rtausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Altschul S.F., Zeeberg B., Earner A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubbs R.A.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blatesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Generation and initial analysis of more than 15,000 full-length
I "Generation and initial analysis of more than 15,000 full-length
I Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhou G.X., Chao L., Chao J.;
"Kallistatin: a novel human tissue kallikrein inhibitor.
"Kallistation. characterization, and reactive center sequence.";
J. Biol. Chem. 267:25873-25880(1992).
-!- FUNCTION: INHIBITS HUMAN AMIDOLYTIC AND KININGGENASE ACTIVITIES OF HUMAN TISSUE KALLIKREIN. INHIBITION IS ACHIEVED BY PORMATION OF AN EQUINOLAR, HEAT- AND SDS-STABLE COMPLEX BETWEEN THE INHIBITOR AND THE ENZYME, AND GENERALION OF A SMALL C-TERMINAL FRAGMENT OF THE INHIBITOR DUE TO CLEAVAGE AT THE REACTIVE SITE BY TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: MONOMER AND SOME HOMODIMERS.
-!- SUBCELLULAR LOCATION: Secreted.
-!- STSUB SPECIPICITY: Synthesized by liver and secreted in plasma.
-!- PTM: THE N-TERMINUS IS BLOCKED.
-!- PTM: THE N-TERMINUS IS BLOCKED.
-!- MISCELLANEOUS: HEPARIN BLOCK KALLISTATIN'S COMPLEX FORMATION WITH
TISSUE KALLIKREIN AND ABOLISHES ITS INHIBITORY EFFECT ON TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Serpin; Serine protease inhibitor; Plasma; Glycoprotein; Signal. SIGNAL. 1 20
of the human protease inhibitor 4 (kallistatin) gene (PI4)."; Genomics 23:370-378(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO: GO:0005209; F:plasma protein; TAS.
GO:0005515; F:protein binding activity; TAS.
GO: GO:0004869; F:serpin; TAS.
InterPro; IPR000215; Serpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE SERPIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93100304; PubMed=1334488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC014992; AAH14992.1; -. PIR; A49518; A49518.
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Genew; HGNC:8948; SERPINA4.
MIM; 147935; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00284; SERPIN; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00079; serpin; 1
SMART; SM00093; SERPIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 388-403.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Plasma;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE-37313267; PubMed=9169871;
A MEDLINE=37313267; PubMed=9169871;
A Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W., Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A., Bentian K., D., Floceth M., Goffeau A., Hebling U., Heumann K., Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P., Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D., Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M., Portetelle D., Purnealle B., Rechmann S., Rieger M., Rinke M., Rose M., Scherens B., Scholler P., Schwarz S., Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P., Verendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E., Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.; H. Nature 387:87-90(1997).
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MISCELLANBOUS: DELETION CAUSES TELOMERE SHORTENING AND SENESCENCE.
SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
TELOMERASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR THE REPLICATION OF CHROMOSOME TERMINI IN MOST BUKARYOTES. IT ELONGATES TELOMERES. IT A REVERSE TRANSCRIPTASE THAT ADDS SIMPLE SEQUENCE REPEATS TO CHROMOSOME BINDS BY COPYING A TEMPLATE SEQUENCE MITHIN THE RNA COMPONENT OF THE ENZYME.
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
11-SEP-2003 (Rel. 42, Last annotation update)
Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST2 OR YLR318W OR L8543.12.
Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                  (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                . .) (POTENTIAL)
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0
                                                                                                                                                                                                                                           37.0%; Score 54; DB 1; Length 427; 46.4%; Pred. No. 1.2; Live 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lingner J., Hughes T.R., Shevchenko A., Mann M., Lundblad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Reverse transcriptase motifs in the catalytic subunit of
                                                                                                                                                            T -> S (IN REF. 3).
3DBBE7AF956D4DAC CRC64;
                                                     (GLCNAC.
(GLCNAC.
(GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 884 AA
                            REACTIVE BOND.
                                                                                                                                                                                                                                                                                                                                                                                    KALLISTATIN
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MEDLINE=97274210; PubMed=9110970;
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Science 276:561-567(1997)
                                                                                                                                                                                                                                                                    Local Similaricy
nes 13; Conservative
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33
108
157
238
NCBI_TaxID=4932;
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ID TERT_YEAST
AC Q06163;
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CARBOHYD
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CONFLICT
SEQUENCE
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BEYAN T.M., Sperger J.M., Chapman K.B., Cech T.R.;

Bryan T.M., Sperger J.M., Chapman K.B., Cech T.R.;

Proc. Natl. Acad. Sci. U.S.A. 95:8479-8484(1998).

-! FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT THE REPLICATION OF CHROMOSOME ENDS BY COPYING A TEMPLATE SEQUENCE MITHIN THE RNA COMPONENT OF THE ENZYME.
                                                                                                                                                                                                                                                                                               Gaps
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InterPro; IPR003545; Telomerase RT.
PRINTS; PR01365; TELOMERASERT.
Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
                                                                                                                                           Pfam, PF00078; rvt; 1.
PRINTS; PR01365; TELOMERASERT.
Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
TELOMERASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.9%; Score 51; DB 1; Length 1132; 39.1%; Pred. No. 8.8; tive 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                         Length 884;
                                                                                                                                                                                                                                                                                               7; Indels
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                                                                                                                                                                                                                     884 AA; 102663 MW; 788334BB49592340 CRC64;
                                                                                                                                                                                                                                                       37.0%; Score 54; DB 1; 36.4%; Pred. No. 2.4; vative 7; Mismatches '
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1132 AA.
or send an email to license@isb-sib.ch)
                                                                   SGD; S0004310; EST2.
GO; GO:0005730; C:nucleolus; IDA.
Interpro; IPR000477; RVTse.
Interpro; IPR003545; Telomerase_RT.
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                                                                                                                                                                                                                                                                                                                             3 FLHWLMSVYVVELLRSFFYVTE 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subunit) (Telomerase subunit P133)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF060230; AAC39163.1; -.
                                     EMBL; U20618; AAB64520.1; -.
                                                                                                                                                                                                                                                                                             8; Conservative
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                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                    DNA-binding
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076332;
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RACALLE-21844401; PubMed=11859360;

RA SQUUCGO V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA SQUUCGO V., Feat N., Hayles J., Bashem D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Gonlins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gonlins M., Connor R., Cronin N., Harris D., Hiddson G.,

RA Gones L., Jones M., Leather S., Huckle E.J., Hunt S., Jagels K.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA Holroyd S., Moules M., Jones M., Leather S., McDonald S., McLean J.,

RA Holroyd S., Moules M., Saunders D., Seeger K., Sharp S.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Rutherford K., Simmonds M., Squares S., Stevens K.,

RA Retlon J., Simmonds M., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Holylor R., Taylor R.G., Holzer E., Moestl D., Hilbert H.,

RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Golffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Locas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,

A Locas M., Revuelta J.L., Moreno S., Armetrong J., Forsburg S.L.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Galibert E., Lower T., McCombie W.R., Paulsen I., Potashkin J.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;

RT H. He genome sequence of Schizosaccharomyces pombe.";

RA Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Ctr6, a vacuolar membrane copper transporter in Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22336382; PubMed=12244050;
Bellemare D.R., Shaner L., Morano K.A., Beaudoin J., Langlois R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pombe.";

J. Biol. Chem. 277:46676-46686 (2002).

I. Biol. Chem. 277:46676-46686 (2002).

I. FUNCTION: Mobilizes stored copper from the vacuole to the cytoplasm under conditions of copper limitation.

I. SUBGINIT: Homotrimer.

I. SUBCELLIULAR LOCATION: Integral membrane protein. Vacuolar.

INDUCTION: By copper deprivation.

SIMILARITY: BELONGS TO THE SLC31A FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION, SUBUNIT, SUBCELLULAR LOCATION, AND INDUCTION
                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Copper transport protein ctr6 (Copper transporter 6)
CTR6 OR SPBC23G7.16.
                                                                                                                                                                       148 AA
                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
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2 KFLHWLMSVYVVELLRSFFYVTE
                           28-FEB-2003 (Rel. 41, Created)
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                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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FIGRFAMS; TIGR00710; efflux Bcr CflA; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;

MEDLINE=95350630; Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Wenter J.C.,
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Potential).
-!- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN AS THE DRUG RESISTANCE TRANSLOCASE FAMILY). BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 269:496-512(1995).
-!- FUNCTION: INVOLVED IN SULFONAMIDE (SULFATHIAZOLE) AND
BICYCLOMYCIN RESISTANCE. PROBABLE MEMBRANE TRANSLOCASE
                                                                                                                                 Length 148;
                                                                                                                                                         8; Indels
PIR; T39949; 13577.16; -.
GeneDB SPombe; SPBC23G7.16; -.
Pfam; PF04145; Ctr; 1.
Transmembrane; Transport; Copper transport.

EXTRACELIULAR (POTENTIAL)
                                                                                             EXTRACELLULAR (POTENTIAL)
D5E214905DBB0491 CRC64;
                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                                                              Score 49; DB 1;
Pred. No. 2.2;
7; Mismatches 8
                                                                                                                                                                                                                                                                                      (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                               1 AKFLHWLMSV----YVVELLRSFFYVTETTFQ 28
                                                                                                                                                                                              38 SQFLLSLLAILGYLFERLRSFTSLKETEFQ 69
                                                                                                                                                                                                                                                                                                                             Bicyclomycin resistance protein homolog
                                                                                  POTENTIAL
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InterPro; IPR007114; MFS.
InterPro; IPR005828; Sub_transporter.
Pfam; PF00083; sugar_tr; 1.
                                                                                                                                                                                                                                                                 PRT;
                                                                                                         16747 MW;
                                                                                                                                 33.6%;
40.6%;
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                                                                                                                                                         Conservative
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                                                                                                         148 AA;
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P45123;
                                                                     DOMAIN
TRANSMEM
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Best Local
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MEDLINE=98037514; PubMed=9371463;

MEDLINE=98037514; PubMed=9371463;

MEDLINE=98037514; PubMed=9371463;

Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

Aldredge T., Bashirzadeh R., Lumm W., Pothier B., Qiu D.,

Farrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,

Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,

Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,

McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

Daniels C.J., Mao J. I., Rice P., Noelling J., Reeve J.N.,

"Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH; Euntional analysis and comparative genomics.";
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-! CORACTOR: Binds 1 zinc ion per subunit (By similarity).
-! SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-! SIMILARITY: BELONGS TO PEPTIDASE FAMILY M48.
Transport; Transmembrane; Inner membrane;
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Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 398;
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InterPro; IPR001915; Peptidase M48.
InterPro; IPR006025; Zn_MTpeptdse.
Pfam; PF04135; Peptidase M48; I.
PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
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Pred. No. 8.5;
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36.7%;
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    Antibiotic resistance;
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72
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122
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164
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MEROPS; M48.004; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       398 AA;
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Best Local Similarity
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AC O26669;
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MEDLINE-81053752; PubMed=6159584;
Goeddel D.V., Shepard H.M., Yelverton E., Leung D., Crea R., Sloma A.,
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete amino acid sequence of human fibroblast interferon as deduced using synthetic oligodeoxyribonucleotide primers of reverse
  Zinc; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Isolation and structure of a human fibroblast interferon gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=80254542; PubMed=6157094;
Derynck R., Content J., Declercq E., Volckaert G., Tavernier J.,
Devos R., Fiers W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=81005095; PubMed=6157601;
Taniguchi T., Ohno S., Fujii-Kuriyama Y., Muramatsu M.;
"The nucleotide sequence of human fibroblast interferon cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=81053720; PubMed=6159580;
Houghton M., Eaton M.A.W., Stewart A.G., Smith J.C., Doel S.M.,
Cartlin G.H., Lewis H.M., Patel T.P., Emtage J.S., Carey N.H.,
                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohno S., Taniguchi T.;
"Structure of a chromosomal gene for human interferon beta.";
                                                                   (BY SIMILARITY)
                                                                                            NC (CATALYTIC) (BY SIMILARITY)
DBD9884292ABFA13 CRC64;
                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Interferon beta precursor (IFN-beta) (Fibroblast interferon)
                                                                                                                                    Length 258;
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                             7; Indels
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"Synthesis of human fibroblast interferon by E. coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lawn R.M., Adelman J., Franke A.E., Houck C.M., Gross
Najarian R., Goeddel D.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Human fibroblast interferon gene lacks introns.";
Nucleic Acids Res. 9:1045-1052(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 78:5305-5309(1981).
                                                 AINC (CATALYTIC) (E
BY SIMILARITY.
ZINC (CATALY
                                                                                                                                    DB 1:;
                                                                                                                                           7.7;
                                                                                                                                                                                                                                                                                 187 AA.
 Metalloprotease;
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                                                                                                                                   Score 47;
Pred. No.
                                      POTENTIAL.
POTENTIAL.
ZINC (CATA
BY SIMILAR
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                                                                                                                                                                                                     PRT;
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21-JUL-1986 (Rel. 01, Last seg
                                                                                                       28605 MW;
                                                                                                                                   32.2%;
  Hydrolase;
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                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                            IFNB1 OR IFNB OR IFB.
Homo sapiens (Human).
                                                                                        150 1
258 AA;
                                                                                                                                               Similarity
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 Transmembrane;
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P01574;
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Matches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98004481, PubMed=321320.

Karpusas M., Nolte M., Benton C.B., Meier W., Lipscomb W.N., Goelz S., "The crystal structure of human interferon beta at 2.2-A resolution.", Proc. Natl. Acad. Sci. U.S.A. 94:11813-11818 (1997).

-!- FUNCTION: HAS ANTIVIRAL, ANTIBACTERIAL AND ANTICANCER ACTIVITIES.

-!- SUBGUIT: Monomer.

-!- SUBCLIULIAR LOCATION: Secreted.

-!- PHARMACEUTICAL: Available under the names Avonex (Bioqen),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.040; -. Gextracellular; IC. GO:0005576; C:extracellular; IC. GO:0005380; F:antiviral response protein activity; NAS. GO:0005132; F:interferon-alpha/beta receptor ligand activity; NAS. GO:0030236; P:anti-inflammatory response; NAS. GO:0042100; P:B-cell proliferation; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WWW="http://www.avonex.com/".
DATABASE: NAME=Betaseron; NOTE=Clinical information on Betaseron;
WWW="http://www.betaseron.com/betas/index.jsp".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ō
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHARMACEUTICAL: Available under the names Avonex (Biogen), Betaseron (Berlex) and Rebif (Serono). Used in the treatment of multiple sclerosis (MS). Betaseron is a slightly modified form of IFNB1 with two residue substitutions.
                                                                                                      ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shepard H.M., Leung D., Stebbing N., Goeddel D.V.; "A single amino acid change in IFN-betal abolishes its antiviral
                                                                                                                                                                                                  MEDLINE-81053854; PubMed-6159597; Houghton M., Stewart A.G., Doel S.M., Emtage J.S., Eaton M.A.W., Smith J.C., Patel T.P., Lewis H.M., Porter A.G., Birch J.R., Carey N.H.; Cartwright T., Carey N.H.; "The amino-terminal sequence of human fibroblast interferon as deduced from reverse transcripts obtained using synthetic oligonucleotide primers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DATABASE: NAME=Avonex; NOTE=Clinical information on Avonex;
                                                        MEDLINE=86035565; PubMed=2414376;
May L.T., Sehgal P.B.;
"On the relationship between human interferon alpha 1 and beta
                                                                                                                                                                                                                                                                                                                                                                                                                                              "Assignment of the disulphide bonds of leukocyte interferon."; Nature 289:606-607(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 71-187 FROM N.A. (VARIANT CLONE PF526).
MEDLINE=82080683; Pubmed=6171735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 8:1913-1931(1980) .
  Nucleic Acids Res. 8:4057-4074(1980).
                                                                                                                                          Interferon Res. 5:521-526(1985)
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=81123083; PubMed=6162107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; V00534; CAA23795.1; -.
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                                                                                                                                                                               SEQUENCE OF 1-68 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 294:563-565(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A93721; IVHUB1.
PDB; 1AU1; 17-JUN-98.
Genew; HGNC:5434; IFNB1.
MIM; 147640; -.
                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  DISULFIDE BOND
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01-FEB-1994
30-MAY-2000
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                     TAS.
GO:0006919; P:caspase activation; NAS.
GO:0001166; P:call surface receptor linked signal transdu. . .; TV
GO:0003101; P:natural killer cell activation; NAS.
GO:0008285; P:negative regulation of cell proliferation; NAS.
GO:0046597; P:negative regulation of virion penetration; NAS.
GO:0046599; P:positive regulation of innate immune response; NAS.
GO:0046543; P:response to viruses; NAS.
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                                                                                                                                                                                                                                                                                                                                                       C -> Y (IN CLONE PF526, LOSS OF ABILITY
TO PORM THE ESSENTIAL DISULFIDE BOND,
LOSS OF ANTIVIRAL ACTIVITY).
FFIG=VAR 004016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95074921; PubMed=7983761; Stamey F.R., Pellett P.E.; Stamey F.R., Dominguez G., Black J.B., Dambaugh T.R., Pellett P.E.; Stamey F.R., Dominguez G., Black J.B., Dambaugh T.R., Pellett P.E.; Surmey F.R., Dominguez G., Elschidton of human herpesvirus 6B oxiLyt suggests acquisition of oriLyt by transposition."; J. Virol. 65:589-596(1995).
-! SUBCELLULAR LOCATION: Integral membrane protein.
-! SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                                                                                                                                                                          PROSITE; PS00252; INTERFERON A B D; 1.
Cytokine; Glycoprotein; Antiviral; Signal; Pharmaceutical;
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Pred. No. 7.8;
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                                                                                                                                                                                                                                                                                                    INTERFERON BETA.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human herpesvirus (type 6 / strain 229) (HHV6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-0CT-2001 (Rel. 34, Last sequence update) 6-protein coupled receptor homolog U51.
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                                                                                                                                          InterPro; IPR000471; Interferon abd.
Pfam; PF00143; interferon; 1.
PRINTS; PR00266; INTERFERONAB.
ProDom; PD000550; Interferon abd; 1.
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(Rel. 34, Last seq
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28.0%;
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01-OCT-1996
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CARBOHYD
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VUS1_HSV6Z
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(See http://www.isb-sib.ch/announce/
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MEDLINE=93114603; PubMed=8417993;
Crozier N.H., Crozier Y.C.;
Crozier R.H., Crozier Y.C.;
The mitochondrial genome of the honeybee Apis mellifera: complete sequence and genome organization.";
Genetics 133:97-117(1993).
-:- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
Apidae; Apis.
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
S (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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30-MAY-2000 (Rel. 39, Last annotation update)
NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3).
                                                                                                PIR; T44011; T44011.
InterPro; IPR000276; GPCR Rhodpsn.
PROSITE; PS00237, G_PROTEIN_RECEP_F1_1; FALSE_NEG_PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-profein coupled receptor; Transmembrane.
DOMAIN
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4; Mismatches
                                                                                                                                                                                                                                                 1 (POTENTIAL)
                              send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46;
Pred. No.
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InterPro; IPR0013916; NADHub_oxred5.
InterPro; IPR001750; Oxidored_q1.
InterPro; IPR001516; Oxidored_q1.
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(Rel. 28, Last seq
                                                                         EMBL; AF157706; AAB06349.1; -.
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                                                            31.5%; Score 46; DB 1; Length 554; 47.4%; Pred. No. 24; tive 5; Mismatches 5; Indele
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Pfam; PF00161; oxidored_q1; 1.
Pfam; PF00662; oxidored_q1 N; 1.
PRINTS: PR01434; NADHDHGNASES:
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 554 AA; 65590 MW; 0C0ECCB99CD756E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00361; oxidored q1; 1.—Pfam; PF00662; oxidored q1; 1.—Pfam; PF01434; NaDHDHONĀES.
Oxidoreductaes; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 570 AA; 65196 MW; 23636CFDC1B0BC4C CRC64;
                                                                                                                                                                                           01.APR-1990 (Rel. 14, Created)
1.APR-1990 (Rel. 14, Last sequence update)
01.FEB-1996 (Rel. 33, Last annotation update)
NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3).
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InterPro; IPR003916; NADHub oxred5.
InterPro; IPR001750; Oxidored_q1.
InterPro; IPR001516; Oxidored_q1.
                                                                                                   3 FLHWLMSVYVVELLRSFFY 21
                                                                                                                16 FLMMLMSLYLLYLNKEFFF 34
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                                                   Query Match
Best Local Similarity 47.4%
Best Local 9, Conservative
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Best Local Similarity
7; Conserva
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                        Mitochondrion.
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095573;
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16-0CT-2001
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ID NUSM P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           synthetase 3 gene.";

Gene 278:185-192(2001).

-!- FUNCTION: ACTIVATION OF LONG-CHAIN FATTY ACIDS FOR BOTH SYNTHESIS

OF CELLULAR LIPPIDS, AND DEGRADATION VIA BETA-OXIDATION.

PREFERENTIALLY USES MYRISTATE, LAURATE, ARACHIDONATE AND ERCARPENTARNOATE AS SUBSTRATES (BY SIMILARITY).

-!- CATALYIC ACTIVITY: A long-chain carboxylic acid + CoA = AMP + diphosphate + an acyl-coA.

-!- COFACTOR: MAGNESIUM (BY SIMILARITY).

-!- COFACTOR: MAGNESIUM (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: MICROSOMES, OUTER MITOCHONDRIAL MEMBRANE

AND PEROXISOMAL MEMBRANA.

-!- SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97321062; PubMed=9177793; Minekura H., Fujino T., Endo Y., Yamamoto T.T.; Minekura H., Fujino T., Kang M.-J., Fujita T., Endo Y., Yamamoto T.T.; "Human acyl-coenzyme A synthetase 3 cDNA and localization of its gene (ACS3) to chromosome band 2q34-q35.";
28-FEB-2003 (Rel. 41, Last annotation update)
Long-chain-fatty-acid--CoA ligase 3 (EC 6.2.1.3) (Long-chain acyl--CoA synthetase 3) (LACS 3).
FACL3 OR ACS3 OR LACS3.
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MEDLINE=21564184; PubMed=11707336;
Minekura H., Kang M.-J., Inagaki Y., Suzuki H., Sato H., Fujino T.,
Yamamoto T.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genomic organization and transcription units of the human acyl-CoA
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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60, GO:004321; ARLTY-acyl-COA synthase activity; TAS.
InterPro: IPRO0873; AMP-bind.
Pfam; PF00501; AMP-binding; 1.
PRINTS; PR00154; AMPENINDING.
PROSITE; PS00455; AMP BINDING; 1.
Ligase; Fatty acid mctabolism; Magnesium; Multigene family.
SEQUENCE 720 AA; 80345 MW; 845959A765BC6BF6 CRC64;
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FIHFLISLYTILTYIPFYFFSES 47
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EMBL; AB061712; BAB72074.1; -.
Genew, HGNC.3570; FACL3.
MIM; 602371; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics 42:180-181(1997).
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O9mnk3 galathealin
Q9en28 amsacta moo
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Q8i8z7 sterkiella
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     28i2w8 plasmodium
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MRR-2003 (TrEMBLrel. 23, Last annotation update)
ABG-deleted variant of telomerase reverse transcriptase.
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Q8n6c3 homo sapien
Q8ne66 homo sapien
Q9dx24 mesocricetu
Q9de32 xenopus lae
Q9pet2 candida alb
Q9pet2 candida alb
Q9pet3 candida alb
Q9bet3 candida alb
Q9pet3 candida nov
Q9jk99 rattus norv
Q8sqq0 encephalito
C55774 schizosacch
Q8cRG dictyosteli
Q9218 rickettsia
Q9218 rickettsia
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Copyright (c) 1993 - 2003 Compugen Ltd.
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No.
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SEQUENCE FROM N.A.

**MEDLINE=21240330; PubMed=11342218;
Guo W., Okamoto M., Lee Y.M., Baluda M.A., Park N.H.;

"Enhanced activity of cloned hamster TERT gene promoter in transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO1365; TELOMERASERT.
RNA-directed DNA polymerase; Transferase.
SEQUENCE 1128 AA; 128394 MW; 1D4F81249012174E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Kuramoto M., Ishikawa F.;

"Telomerase reverse transcriptase of Xenopus laevis.";

Submitted (BEC-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF212299; AAG43537.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 16, Last sequence update) (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 122; DB 11;
Pred. No. 7.5e-10;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 113; DB 13;
Pred. No. 1.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1191 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                          Biochim. Biophys. Acta 1517:398-409(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   536 AVFLFWLMDAYVVELLRSFFYVTETTFQ 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKFLHWLMSVYVVELLRSFFYVTETTFQ
  Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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01-MAR-2001 (TrEMBLrel. 16, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
                                                                                                                                                                                                                                                                                                                              EMBL, AF149012; ART134.1; -
INTERPRO, IPRO00477; RVTSe.
INTERPRO, IPRO03545; Telomerase RT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Telomerase reverse transcriptase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 77.4%;
1 Similarity 71.4%;
20; Conservative 4
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Best Local Similarity 85.7%;
Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00078; rvt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                 NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002 (
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01-MAR-2003 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                       Kazumasa H.;
"Both beta and gamma deletion isoform of human telomerase reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 146; DB 4; Length 807; 100.0%; Pred. No. 1.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Hisatomi H., Nagao K., Hirata H., Hikiji K., Kanamaru T.,
"Exon II deleted variant of the human telomerase reverse
transcriptase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AB085628; BAC11010.1; -.
InterPro; IPR002545; Telomerase_RT.
PRINTS; PR01365; TeLOMERASET.
RNA-directed DNA polymerase.
SEQUENCE 1069 AA; 120047 MW; BEIE77A653B1C666 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AB086379; BAC11014.1; -. InterPro; IPR001545; Telomerase RT. PR0155; TeLOMERASER RT. SEQUENCE 807 AA, 90225 WW; 199664460CE6D763 CRC64;
                                                         Beta and gamma deletion isoform of telomerase reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9QXZ4 PRELIMINARY; PRT; 1128 AA. 090XZ4; Clarent 13, Created) Clarent 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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100.0%; Pred. No. 1.7e-13;
iive 0; Mismatches 0;
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Matches 28; Conservative
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Matches 28; Conservative
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                                                                                                                                                                                                                                                                                                             TISSUE=Stomach cancer;
                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 transcriptase."
                                                                                         transcriptase.
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OBNG46; Q8NG46

RESULT 3 08NG46

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Telomerase reverse transcriptase.

Telomerase catalytic subunit.

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Gaps

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Metz A.M., Love R.A., Strobel G.A., Long D.M.; "Two Expressed Telomerase Reverse Transcriptase Genes Identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oguchi K., Tamura K., Takahashi H.;
"Molecular cloning and characterization of OsTERT, a telomerase reversee transcriptase homolog in Oryza sativa.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF288216; AAK35007.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 61; DB 10; Length 1259; Pred. No. 1.4;
                                                                                                                                                                                                                                                                        Score 63, DB 3; Length 867; Pred. No. 0.5; 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR01365; TELOMERASERT.
PROSITE; PS00527; RIBOSOMAL S14; 1.
RNA-directed DNA polymerase; Transferase.
SEQUENCE 1259 AA; 143710 MW; 15B041789F2D5CAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                              Candida albicans.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
BMBL, AF216811, AAF26732.1;
InterPro; IRRN00477; RVTse.
Pfam; PF00078; rvt; I.
RNA-directed DNA polymerase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                     3 FLHWLMSVYVVELLRSFFYVTETT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
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InterPro; IPR0000477; RVTEG.
InterPro; IPR003545; Telomerase_RT.
Pfam; PF00078; rvt; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Telomerase reverse transcriptase
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                                                                                                                                                                                                                                                                          43.2%;
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QBLKW0;
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                      Local Similarity 45.8 es 11; Conservative
                  Candida albicans (Yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gramene; Q9AU13;
                                                              NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4530;
                                                                                                          STRAIN=3153;
                                                                                                                                                                                                                                                                        Query Match
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Q8LKW0
1D Q8LKW
AC Q8LKW
DT 01-OC
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                                                                                    SEQUENCE FROM N.A. Wang L., Dean S.R., Shippen D.E.; "Oligomerization of the Telomerase Reverse Transcriptase from Euplotes
                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI_TaxID=5476;
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                             Eukaryota; Alveolata; Ciliophora; Spirotrichea; Hypotrichia;
Euplotida; Euplotidae; Moneuplotes.
                                                                                                                                                                                                                                                                                      45.2%; Score 66; DB 5; Length 1032; 52.2%; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 43.2%; Score 63; DB 3; Length 867; Local Similarity 45.8%; Pred. No. 0.5; les 11; Conservative 6; Mismatches 7; Indels
                                                                                                                                                                                                                      PRINTS; PR01365; TELOMERASERT.
RNA-directed DNA polymerase; Transferase.
SEQUENCE 1032 AA; 122966 MW; 0C401515839801A8 CRC64;
                                                                                                                                                                                                                                                                                                                    8; Indels
                                                                                                                                 crassus.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF528527, AAM95622.1; -.
InterPro; IPR000477; RVTse.
InterPro; IPR003545; Telomerase_RT.
PFam; PF00078; rvt; 2.
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PRINTS; PR01365; TELOMERASERT.
RNA-directed DNA polymerase; Transferase.
SEQUENCE 867 AA; 100894 MW; 3273E381D5E65062 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Candida albicans.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vi-UCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Telomerase reverse transcriptase 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         867 AA.
                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333 YLWWLFEHLLKNILRSFWYITETS 356
                                                                                                                                                                                                                                                                                                                                                                   3 FLHWLMSVYVVELLRSFFYVTETT 26
                                                                                                                                                                                                                                                                                                                                                2 KFLHWLMSVYVVELLRSFFYVTE 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000477; RVTse.
InterPro; IPR003545; Telomerase_RT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF216872; AAF26733.1;
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Candida albicans (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                   Local Similarity
ses 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=3153;
               uplotes crassus
                                                        NCBI_TaxID=5936;
                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9P8T2
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Matches
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Matches
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Q9P8T2
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Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P., Weissenbach J., Vivares C.P., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P., "Genome sequence and gene compaction of the eukaryote parasite facephalitozoon cuniculi.";

Mature 414.450-453(2001).

EMBL; AL590451; CAD27002.1;

InterPro; IPR00078; RVTse.

EMBL; AL590451; CAD27002.1;

RNA-directed DNA polymerase; Transferase.

SROUENCE 823 AA; 95280 MW; BPDIBED4CCE68354 CRC64;
                                                                                                                                                    Eukaryota, Fungi, Microsporidia, Unikaryonidae, Encephalitozoon.
NCBL_TaxID=6035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lyne M., Rajandream M.A., Barrell B.G., Oliver K., Harris D.; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AL022598; CAA18644.1; -.
GeneDB SPOMDE, SPCC1795.09; -.
InterPro; IPRO01461; AspproteaseA1.
Pfam; PP00026; asp; 1.
PRINTS; PR00792; PEPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.6%; Score 53.5; DB 3; Length 521; 34.4%; Pred. No. 8.4; tive 7; Mismatches 9; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.7%; Score 55; DB 5; Length 823; 29.6%; Pred. No. 7.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                           Genoscope,
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     521 AA; 57623 MW; 21F002CF829175EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                  (TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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823 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             521 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326 SRFLVYITEKLIIPIISKYFYCTETSF 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AKFLHWLMSVYVVELLRSFFYVTETTF 27
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21576510; PubMed=11719806;
                                                                                                  Telomerase reverse transcriptase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 29.69
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 34.4 nes 11, Conservative
PRELIMINARY;
                                                                                                                                     Encephalitozoon cuniculi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aspartic protease.
SPCC1795.09.
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                          STRAIN=GB-M1;
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                                                                                                                                                                                                                                                                                                                                           STRAIN=GB-M1
                    Q8SQQ0;
01-JUN-2002
                                                       01-JUN-2002
                                                                              01-MAR-2003
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                       Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnolliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                               STRAIN=cv. Nipponbare;
MBDLINE-2209615.9 PubMed=12100484;
Heller-Uszynska K., Schnippenkoetter W., Kilian A.;
"Cloning and characterization of rice (Oryza sativa L) telomerase reverse transcriptuse, which reveals complex splicing patterns.";
Plant J. 31:75-86 (2002).
EMBL; AP494453; AAM21641.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.7%; Score 58; DB 11; Length 575; 83.3%; Pred. No. 1.9; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO1365; TELOMERASERT.
PROSITE; PS00527; RIBOSOMAL S14; 1.
RNA-directed DNA polymerase; Transferase.
SEOUENCE 1261 AA; 143715 MW; 353153D1C8B7D5CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Wong S., Gao S., Xu X., Yu H.;

"Rat telomerase catalytic subunit, rTERT.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF247818; AAF62177.1;

InterPro; IPR000477; RVTse.

InterPro; IPR003545; Telomerase_RT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      575 AA; 65672 MW; F80C81BD7F6A91A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00078; rvt; 1.
PRINTS; PR01365; TELOMERASERT.
NON TER.
SEQÜENCE 575 AA; 65672 MW; F80C81BD7F
                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000477; RVTse.
InterPro; IPR003545; Telomerase_RT.
Pfam; PF00078; rvt; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             685 WISWLFSDIVIPVVRTYFYVTE 706
                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001209; Ribosomal_S14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 FLHWLMSVYVVELLRSFFYVTE 24
                    felomerase reverse transcriptase
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Best Local Similarity 83.3
Matches 10; Conservative
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1 RSFFYITESTFQ 12
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                                                                                                                                                                                                                                                                                                                                         Gramene; Q8LKW0; -.
                                                                                                                                                                            SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 1 | SEQUENCE FROM N.A.
| SEQUENCE FROM N.A. |
| SEGUENCE FROM N.A. |
| STRAIN-A.Y. |
| A Anjard C. Loomis W.F.; |
| Evolution of the ABC transporters of Dictyostelium."; |
| Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. |
| I. SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. |
| R. EMBL; AF46339; AAL931500.1; -. |
| InterPro; IPR003439; AAA_ATPase. |
| InterPro; IPR003439; ABC_transporter. |
| Section of the ABC transporter. |
| Section of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.6%; Score 52; DB 16; Length 102; 50.0%; Pred. No. 3; tive 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166858 MW; 21425B402BE60F0C CRC64;
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EMBL, AB008621; AAL03140.1; -

Interpro; IPR000516; Ni hydr CytB.

Pfam; PF0129; Ni hydr CyTB; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 102 AA; 11898 MW; D65104E7E81886C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUNA-2003 (TrEMBLrel. 23, Last annotation update)
ABC transporter AbcG15.
ABCG15.
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Last annotation update)
274 KLTHYAVSIYSVQFLNSTFFSNYSIITDAYFQ 305
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ProDom; PD000006; ABC transporter; 2.
SMART; SM00382; AAA; 2.
PROSITE; PS00211; ABC TRANSPORTER; 1.
ATP-binding; Transport.
SEQUENCE 1475 AA; 166858 MW; 2142:
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Matches 14; Conservative
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Matches 8; Conserv
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Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis;
prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human telomerase reverse transcriptase antigenic peptide S-1.
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AAY00648
AAW61349
AAY00643
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AAW46997
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AAW71376
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AAY43621
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96US-0724643.
97US-0844419.
97US-0851843.
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97US-0911312.
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hTERT fragment wit
Amino acid sequenc
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          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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ABG71627
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AAY25461
                                                - protein search, using sw model
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1 FFYVTETTFQKNRLFFYRKSVWSK
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(GERO-) GERON CORP

Result Š.

Morin GB,

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The present sequence represents an antigenic peptide from human telomerase reverse transcriptase (hTRT), from the present invention. The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein preparation of hTRT with a telomerase NNA component; (C) detection of the hTRT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of NNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of hTRT in the sample; and (D) increasing the product with presence of hTRT in the sample; and (D) increasing the product with presence of hTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing the proliferation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polynucleotide encoding hTRT can be used in the manufacture of medicaments for inhibiting the used to treat conditions that are associated with high telomerase crivity. A protein preparation of hTRT can also be used in the new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                       Pure and recombinant human Telomerase Reverse Transcriptase and variants - are useful in the diagnosis, prognosis and treatment cell proliferation conditions especially cancer and ageing
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100.0%; Pred. No. 6.4e-13;
ive 0; Mismatches 0;
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                                                                                                                                                        Chapman KB,
Harley CB;
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                                                                                                            (UYTE-) UNIV TECHNOLOGY CORP.
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"hea 24; Conservative
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                                                                                                                                                        , Cech TR,
Nakamura T,
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  09-MAY-1997;
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                                                                                                                                                           Andrews WH,
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                                                                                                                                                                                                                                                                                The present sequence represents an antigenic peptide from human telomerase reverse transcriptase (HTRT), from the present invention. The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein preparation of hTRT with a telomerase RNA component; (C) detection, amplifying the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of hTRT in the sample; and (B) increasing the product with presence of hTRT in the sample; and (B) increasing the proliferation of a vertebrate cell by increasing hTRT can be used in the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polynucleotide encoding hTRT can be used in the manufacture of medicaments for inhibiting the cleffect of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions that are associated with high telomerase
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prognosis; cell proliferation; cancer; ageing; ribonucleoprotein;
                                                                                                                                                      Pure and recombinant human Telomerase Reverse Transcriptase and variants - are useful in the diagnosis, prognosis and treatment cell proliferation conditions especially cancer and ageing
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                                               Lingner J;
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                                            Harley C,
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                                            Chapman KB,
Harley CB;
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(UYTE-) UNIV TECHNOLOGY CORP.
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es 24; Conservative
                                          , Cech TR,
Nakamura T,
                                                                                                            WPI; 1998-171633/16.
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18-APR-1997;
25-APR-1997;
06-MAY-1997;
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Sequence Query Match Best Loc Matches antigenic Synthetic

AAW57387;

RESULT 2 AAW57387

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Saeterdal I;

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especially, breast, lung, ovarian, cervical, colorectal, prostate or parcreatized cancers, malignant melanoma, leukaemias, lymphomas, or biliary tract carcinomas. They are useful for generating telomerase Tlymphocytes capable of recognising and destroying tumour cells in a mammal, comprising culturing Tlymphocytes obtained from the mammal with the peptides. Telomerase protein is expressed only by tumour cells hence, other body cells are not targeted or destroyed by telomerase specific T
                                                                                                                        Protein or peptide fragments useful in the treatment and prophylaxis of cancer in mammals -
                                                                                                                                                                                                                                                                                                                                                                   cells.
Note: This sequence was indexed from WO200002581, which is the first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; telomerase catalytic subunit; hTERT; human leukocyte antigen; human telomerase reverse transcriptase; HLA epitope; cancer; HLA profile; breast cancer; pancreatic cancer; colorectal cancer; lung cancer; malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma; anti-cancer; mutant; cytostatic; HLA class I epitope; HLA class II epitope; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hTERT fragment with HLA containing polypeptide at its N-terminus.
                                                                                                                                                                                                      This sequence represents a telomerase peptide of the invention, be used in a method for the treatment or prophylaxis of cancer sequences are useful in the treatment or prophylaxis of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                              Gjertsen MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 131; DB 21; 100.0%; Pred. No. 1.3e-12;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 major country equivalent to NO9803141.
                                            Moller M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Moller M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 FFYVTETTFQKNRLFFYRKSVWSK 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FFYVTETTFØKNRLFFYRKSVWSK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG71627 standard; protein; 100 AA.
                                                                                                                                                                        Claim 9; Page 34; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-FEB-2002; 2002WO-NO00069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAR-2001; 2001GB-0005238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eriksen JA, Gaudernack G,
                                              Eriksen JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24; Conservative
              (NHYD ) NORSK HYDRO AS
                                                                                           WPI; 2000-145727/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEMV-) GEMVAX AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                  48 AA;
                                                             Saeboe-Larsen S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200270679-A2.
                                              Gaudernack G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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ABG71627
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New polypeptide with an additional C-terminal and/or N-terminal

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The present invention relates to a polypeptide comprising a 20 amino acid sequence derived from human telomerase catalytic subunit for human telomerase reverse transcriptase, hTERT) amino acid sequence for human telomerase reverse transcriptase, hTERT) amino acids and at least two human leukocyte antigen (HiA) class I or class II or class II or amino acid peptide sequence as additional C- and/or N-terminal sequences on a fragment of hTERT which is not more than 100 amino acid peptide sequence as additional C- and/or N-terminal sequences on a fragment of hTERT which is not more than 100 amino acids of hTERT. The polypeptides of the invention are useful in a cancer in population or in a vaccine for preventing or treating cancers such as breast, pancreatic, colorectal, lung, ovarian or carcical cancer, malignant melanoma, leukaemia, lymphoma or biliary tract carcinoma. The polypeptides or encoding polymclectide cancer in a polypeptides or encoding polymclectide sequence are useful for performing identity, sequence homology and/or hybridisation studies, for predicting structure and/or function (e.g. anti-cancer activity), or for screening methods in the sequence as hTERT fragment with the 20 amino acid HLA epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New catalytic protein of telomerase of a higher animal and a gene coding it - useful for diagnosis of diseases caused by the change in activity of a telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The specification describes a human catalytic telomerase protein. The products are useful in drug compositions for the diagnosis of diseases caused by the change in activity of telomerase. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
sequence, useful for preparing anti-cancer vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 131; DB 23;
100.0%; Pred. No. 2.8e-12;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                containing polypeptide at its N-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 FFYVTETTFQKNRLFFYRKSVWSK 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FFYVTETTFOKNRLFFYRKSVWSK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 14; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW97385 standard; Protein; 131 AA
                                    Disclosure; Fig 1; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 24; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MITU ) MITSUBISHI CHEM CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP11046768-A
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ઠે 엄 RESULT 6 AAW46998

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This sequence represents the human telomerase reverse transcriptase (hTERT). The invention relates to a monoclonal antibody recognising the hTERT. The antibody can be used for the investigation, diagnosis and treatment of telomerase-related diseases, especially diseases in which
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hTRT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions that are associated with high telomerase activity. A protein preparation of HTRT can also be used in the new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human telomerase reverse transcriptase; hTERT; antibody; diagnosis; telomerase-related disease; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 283;
                                                                                                                                                               Length 259;
                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        telomerase expression is up-regulated e.g. cancers
                                                                                                                                                         100.0%; Score 131; DB 19;
100.0%; Pred. No. 7.7e-12;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 131; DB 20;
100.0%; Pred. No. 8.5e-12;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Furuya A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human telomerase reverse transcriptase.
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                                                                                                                                                                                                                                           24
                                                                                                                                                                                                                                                                    12 FFYVTETTFQKNRLFFYRKSVWSK 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 72-73; 78pp; Japanese
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                                                                                                                                                                                                                                           1 FFYVTETTFOKNRLFFYRKSVWSK
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                                                                                                                                                                                                                                                                                                                                                                                      AAY43128 standard; Protein; 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-JP01557.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                              Local Similarity 100.
ses 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-591316/50
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283 AA;
                                                                                                                       259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-1998;
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                                                                                                                       Sequence
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                                                                                                                                                             Query Match
                                                                               methods
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a human telomerase reverse transcriptase (hTRT) protein from a cDNA clone from the present invention. The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein preparation of hTRT with a telomerase BNA component; (C) detection of the hTRT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex (D) increasing the product with presence of hTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTRT ceasing the proliferation to agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polynucleotide encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                           Human telomerase reverse transcriptase protein from cDNA clone 712562
                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
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                                                                                                                       ..
                                                                             Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harley C, Lingner J;
                                                                                                                       Indels
                                                                             100.0%; Score 131; DB 20;
100.0%; Pred. No. 3.8e-12;
ive 0; Mismatches 0;
  present sequence appears in the specification.
                                                                                                                                                                                      FYVTETTFQKNRLFFYRKSVWSK 42
                                                                                                                                                             1 FFYVTETTFOKNRLFFYRKSVWSK 24
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Harley CB;
                                                                                                                                                                                                                                                                                                    AAW46998 standard; Protein; 259 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 19; 387pp; English
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97US-0844419.
97US-0851843.
97US-0851843.
97US-0911312.
97US-0912951.
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                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1998 (first entry)
                                                                                                Local Similarity 100.
les 24; Conservative
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Nakamura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-171633/16
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                                          131 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996;
18-APR-1997;
25-APR-1997;
06-MAY-1997;
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14-AUG-1997
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                                                                                                                                                                                                   19
                                                                                                                                                                                                                                                                                                                                              AAW46998;
                                          Sequence
                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                   proteins containing a reverse transcriptase motif, which act as telomerase inhibitors. The gene, its encoded protein and derived antibodies can be used to provide base sequence information, detect telomerase activity and cancer cells, and to screen telomerase inhibitors. The detection method is simple and effective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human telomerase reverse transcriptase 63 kDa clone 712562 protein.
                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel human CRT-1 genes and their encoded
                                                                                                                                                                                                                                                                                                            Novel gene, useful in detection of telomerase activity and cancer cells as well as screening telomerase inhibitors for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
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            /note= "Partial sequence, no stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 438;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 131; DB 20; 100.0%; Pred. No. 1.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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/label= encoded by ARG
                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 35-36; 44pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FFYVTETTFOKNRLFFYRKSVWSK 24
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0
/label= CRT-1
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96US-0724643.
97US-0844419.
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                                                                                                                                                     98JP-0013232.
                                                                                                         99WO-JP00039
                                                                                                                                      98JP-0139177
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                                                                                                                                                                                                  (CHUS ) CHUGAI SEIYAKU KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24; Conservative
                                                                                                                                                                                                                                 Yoshida K;
                                                                                                                                                                                                                                                                WPI; 1999-430393/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438 AA;
                                                                                                                                                                                                                                                                                N-PSDB; AAX88250
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01-OCT-1996;
18-APR-1997;
                                                                                                                                                     08-JAN-1998;
                                             WO9935261-A1
                                                                                                         38-JAN-1999;
                                                                                                                                      06-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1997;
                                                                                                                                                                                                                                 Tsuchiya M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB2317891-A
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                                                                          15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW56109,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                              cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins containing a reverse transcriptase motif, which act as telomerase inhibitors. The gene, its encoded protein and derived antibodies can be used to provide base sequence information, detect telomerase activity and cancer calls, and to screen telomerase inhibitors. The detection method is simple and effective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel human CRT-1 genes and their encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel gene, useful in detection of telomerase activity and cancer cells as well as screening telomerase inhibitors for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRT-1; reverse transcriptase; telomerase; inhibitor; detection; telomerase activity; cancer cell; screening; human.
                                                                         CRT-1; reverse transcriptase; telomerase; inhibitor; detection; telomerase activity; cancer cell; screening; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                   1..437
/label= CRT-1
/note= "Partial sequence, no stop codon given"
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100.0%; Pred. No. 1.3e-11;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SO FFYVTETTFOKNRLFFYRKSVWSK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 31-32; 44pp; Japanese.
                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY25462 standard; Protein; 438 AA
                                                                                                                                                                                                                                                                                             99WO-JP00039
                                                                                                                                                                                                                                                                                                                            98JP-0139177.
                                                                                                                                                                                                                                                                                                                                          98JP-0013232.
              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                        (CHUS ) CHUGAI SEIYAKU KK.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Tsuchiya M, Yoshida K;
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                                           Human CRT-1 protein #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-430393/36.
N-PSDB; AAX88243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         437 AA;
                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                 WO9935261-A1
                                                                                                                                                                                                                                                                                             08-JAN-1999;
                                                                                                                                                                                                                                                                                                                            06-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                          08-JAN-1998;
              22-SEP-1999
                                                                                                                                                                                                                                                                15-JUL-1999
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This sequence is a truncated human telomerase of the invention. Primers that amplify the telomerase coding sequence can be used in a method for diagnosing cancer in a patient. The telomerase can be used for detection, diagnosis and drug screening. Inhibitors of telomerase activity can be used to treat cancers such as melanomas, other skin cancers, meuroblastomas, breast carcinomas, colon carcinomas, leukaemias, lymphomas, osteosatromas or smooth muscle cell hyperplasias or skin growths. Enhancers of telomerase may be used to stimulate stem cell proliferation and differentiation (expansion of haematopoidic tem well, many tissues have stem cells. Proliferation of these cells may be tumour, organ regeneration or differentiation after the second such as wilm's tumour, organ regeneration or differentiation after injury or diseases, nerve cell or brain cell growth following injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Telomerase; human; cancer; diagnosis; melanoma; skin cancer, leukaemia; neuroblastoma; breast carcinoma; colon carcinoma; Iymphoma; osteosarcoma; smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour; stem cell differentiation; organ regeneration; organ differentiation.
                                                                                                                                                                                                                                                                                                                                                                    New isolated vertebrate telomerase genes - used to develop products for treating cancers or for organ regeneration, nerve cell or brain cell growth following injury or bone marrow transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-terminal truncated telomerase (ver. 2) protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 131; DB 20;
100.0%; Pred. No. 1.8e-11;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         560 FFYVTETTFOKNRLFFYRKSVWSK 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FFYVTETTFOKNRLFFYRKSVWSK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY00644 standard; Protein; 588 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Fig 11a; 134pp; English.
                                                                                                                                                                                                                 BIOSYSTEMS LLC
                                                                                   97US-0058287.
97US-0051410.
97US-0053018.
97US-0053329.
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                                                                                                                                                                         97US-0054642
                                          98WO-US13835
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Bust Local Similarity luv...
Annes 24; Conservative
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                                                                                                                                                                                                                                                              D, Kilian A;
                                                                                                                                                                                                                                                                                                       WPI; 1999-106060/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                588 AA;
                                                                                                                                                                                                                                                                                                                             N-PSDB; AAX18263
                                                                                                                                                                                                                   (CAMB-) CAMBIA
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                                          01-JUL-1998;
                                                                                                                                                                         04-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUL-1999
                                                                                                         01-JUL-1997;
                                                                                                                              21-JUL-1997;
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  14-JAN-1999.
                                                                                     09-SEP-1997
                                                                                                                                                    21-JUL-1997
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                                                                                                                                                                                                                                                              Bowtell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a human telomerase reverse transcriptase (hTRT) clone protein from the present invention. The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein of preparation of recombinant telomerase BNA component; (C) detection of the hTRT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of Complex or amplification product with presence of hTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTRT expression; and (E) the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polynucleotide encoding hTRT can be used in the manufacture of medicaments for inhibiting the used to treat conditions that are associated with high telomerase contactivity. A protein preparation of hTRT can also be used in the new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia; neuroblastoma; breast carctinoma; colon carctinoma; orgeosarroma; smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour; stem cell differentiation; organ regeneration; organ differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                         Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 131; DB 19;
100.0%; Pred. No. 1.7e-11;
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                                                                                                                                                                                             Harley C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24
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G.B.
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Harley (
97US-0846017.
97US-0851843.
97US-0854050.
                                                                                                                                                    UNIV TECHNOLOGY CORP
                                                               97US-0911312.
97US-0912951.
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                                                                                                                                                                           Cech TR, C
                                                                                                                                                                                                                 Nakamura
                                                                                                                                                                                                                                                          WPI; 1998-171633/16.
N-PSDB; AAV22426.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        564 AA;
                                                                                                                              (GERO-) GERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9901560-A1
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                    06-MAY-1997;
                                                                                     14-AUG-1997;
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                                                               14-AUG-1997
                                                                                                                                                                                               Andrews WH,
                                                                                                                                                                                                                   Morin GB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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Query Match

Matches

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Gaps

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and a gene
the change in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel gene, useful in detection of telomerase activity and cancer cells as well as screening telomerase inhibitors for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRT-1; reverse transcriptase; telomerase; inhibitor; detection; telomerase activity; cancer cell; screening; human.
                                                                                                                                 The present sequence represents a catalytic telomerase protein. The products are useful in drug compositions for the diagnosis of diseases caused by the change in activity of telomerase.
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                                                                                                                                                                                                                                                Length 591;
                                                                                                                                                                                                                                                                                       Indels
                   New catalytic protein of telomerase of a higher animal coding it - useful for diagnosis of diseases caused by activity of a telomerase
                                                                                                                                                                                                                                                  100.0%; Score 131; DB 20; 100.0%; Pred. No. 1.8e-11;
                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                19 FFYVTETTFQKNRLFFYRKSVWSK 42
                                                                                                                                                                                                                                                                                                                            1 FFYVTETTFOKNRLFFYRKSVWSK 24
                                                                                                Claim 1; Page 11-14; 18pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY25463 standard; Protein; 622 AA
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/label= CRT-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-SEP-1999 (first entry)
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yoshida K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human CRT-1 protein #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-430393/36.
                                                                                                                                                                                                            591 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  622 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAX88251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9935261-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JAN-1999;
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30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tsuchiya M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY25463;
                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY25463
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                                                                                                                                                                                                                                                                                                                                                        This sequence is a truncated human telomerase of the invention. Primers that amplify the telomerase coding sequence can be used in a method for diagnosing cancer in a patient. The telomerase can be used for detection, diagnosis and drug screening. Inhibitors of telomerase activity can be used to treat cancers such as melanomas, other skin cancers, neuroblastomas, breast carcinomas, colon carcinomas, leukaemias, lymphomas, osteosarcomas or semooth muscle cell hyperplasias or skin growths. Enhancers of telomerase may be used to stimulate stem cell proliferation and differentiation (expansion of haematopoietic stem cells could be administered in the bone marrow transplant context). As well, many tissues have stem cells. Proliferation of these cells may be useful in wound healing, hair growth, treatment of disease such as will standard to brain cell growth following injury.

Note: The Neterminus of this sequence can be replaced by the sequences
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                                                                                                                                                                                                                                                New isolated vertebrate telomerase genes - used to develop products for treating cancers or for organ regeneration, nerve cell or brain cell growth following injury or bone marrow transplantation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 131; DB 20;
100.0%; Pred. No. 1.8e-11;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FFYVTETTFOKNRLFFYRKSVWSK 24
                                                                                                                                                                                                                                                                                                                          Claim 4; Fig.11t-u; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW97384 standard; Protein; 591 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A catalytic telomerase protein.
                                                                                                                (CAMB-) CAMBIA BIOSYSTEMS LLC
97US-0058287.
97US-0051410.
97US-0053018.
97US-0053329.
97US-0054642.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     shown in AAY00656-Y00658
                                                                                                                                                     Bowtell D, Kilian A;
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                                                                                                                                                                                         WPI; 1999-106060/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 588 AA;
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                                                                                                                                                                                                              N-PSDB; AAX18272
                       01-JUL-1997;
21-JUL-1997;
21-JUL-1997;
04-AUG-1997;
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The present sequence represents a human telomerase reverse transcriptase (hTRT) variant from the present invention. The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polymucleotide, on administration of the compound; (B) protein or frecombinant telomerase By contacting a protein preparation of frecombinant telomerase By contacting a protein or preparation of hTRT with a telomerase By component; (C) detection of the hTRT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of HTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTRT expression; and (B) the use of an agent that causes an increase in cell vertebrate cell proliferation of hTRT and the polymucleotide encoding HTRT can be used in the manufacture of medicaments for inhibiting the HTRT and the polymucleotide encoding HTRT can be used in the manufacture of telomerase activity can be effect of ageing or cancer. Inhibitors of telomerase activity can be
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                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing
                                                                                                                                                                                                                                                                                                                                                Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
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 Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harley C, Lingner J;
                                    Indels
                                                                                                                                                                                                                                                                                                                Human telomerase reverse transcriptase Delta182 variant.
Query Match 100.0%; Score 131; DB 20; Best Local Similarity 100.0%; Pred. No. 1.9e-11; Matches 24; Conservative 0; Mismatches 0;
                                                                        1 FFYVTETTFOKNRLFFYRKSVWSK 24
                                                                                             50 FFYVTETTFQKNRLFFYRKSVWSK 73
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Harley CB;
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                                                                                                                                                                                                   AAW46997 standard; Protein; 807 AA
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97US-0844419.
97US-0846017.
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(UYTE-) UNIV TECHNOLOGY CORP.
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97US-0854050.
97US-0911312.
97US-0912951.
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Morin GB, Nakamura T,
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25-APR-1997;
06-MAY-1997;
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14-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
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Search completed: November 12, 2003, 19:47:13 Job time : 29.8868 secs

Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence

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CITY: San Francisco
STATE: California
COUTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Townsend and Townsend and Crew LLP
Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Datamers, Torush APPLICANT: Chapman, Karen B. APPLICANT: Chapman, Karen B. APPLICANT: Morin, Gregg B. APPLICANT: Harley, Calvin APPLICANT: Andrews, William H. TITLE OF INVENTION: No. 6093809el Telomerase NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESS: Townsend and Townsend and Crew LLP
                   US-08-854-050-225
US-09-430-333-225
US-09-430-333-225
US-09-675-321-2
US-08-912-951-2
US-08-912-951-2
US-08-912-951-323
US-08-912-951-323
US-08-912-951-323
US-08-912-951-325
US-08-912-951-324
US-08-912-951-314
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 112:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION UNDBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INORMATION:
NAME: Apple, Randolph T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 112, Application US/08851843A patent No. 6093809 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
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                                           FILING DATE: 2: CLASSIFICATION:
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Sequence 5, Appli
Sequence 5, Appli
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Sequence 267, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 5, App
Sequence 217, A
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90.911 Million cell updates/sec
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Sequence 112,
Sequence 113,
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                                                                                                                                                             November 12, 2003, 19:43:50 ; Search time 11.1698 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13,
Sequence 10,
Sequence 10,
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Sequence 30,
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Sequence 6
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/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
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                        GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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US-08-974-549A-232
US-08-94-954-112
US-09-430-323-112
US-08-912-951-113
US-08-912-951-13
US-08-974-549A-30
US-08-974-549A-13
US-08-974-549A-13
US-08-974-549A-13
US-08-974-549A-13
US-08-974-549A-10
US-08-974-549A-10
US-08-974-549A-10
US-08-974-549A-10
US-08-974-549A-101
US-08-974-549A-101
US-08-974-549A-57
US-08-974-549A-57
US-08-974-549A-57
US-08-974-549A-57
US-08-974-549A-57
US-08-974-549A-217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                       328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                   1 FFYVTETTFOKNRLFFYRKSVWSK 24
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
                                           Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0
100.0
100.0
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                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                               Perfect score:
                                                                                                                  OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                Run on:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION WHERE: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
CLASSIFICATION: 536
CLASSIFICATION: 536
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 131; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco CTY: San Francisco CATFE: California COUNTRY: United States of America
                PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-0CT-1997
ATTORNEY AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 232:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
CORRESPONDENCE: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 112, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Makamura, Toru
APPLICANT: Makamura, Toru
APPLICANT: Morin, Gregg B.
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COMPUTER REALABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
01-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid STRANDEDNESS:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-974-549A-232
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APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Galvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: The PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
FILING DATE: 25-APR-1997
                                                                                                                                                                                                   Query Match
100.0%; Score 131; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 24; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR DATE: 25-APT-1997,
PRIOR DATE: 25-APT-1997,
PLING DATE: 06-WAY-1997
PILING DATE: 06-WAY-1997
PRIOR APPLICATION DATA: 06-WAY-1997
PRIOR APPLICATION DATA: 09-WAY-1997
PRIOR APPLICATION DATA: 09-WAY-1997
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PRIOR APPLICATION DATA: BRIOR APPLICATION DATA: BRIOR APPLICATION DATA: BRIOR APPLICATION DATA: BRIOR APPLICATION DATA: APIG-1997
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Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                          : 24 amino acids
amino acid
SEQUENCE CHARACTERISTICS:
                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-851-843A-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                     STRANDEDNESS:
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TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
TITLE OF INVENTION: THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                  Gaps
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0
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CURRENT APPLICATION DATA:
RPLICATION DATA:
RPLICATION DATA:
RPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
RAPELCATION DATA:
APPLICATION: WHERE: US 08/854,050
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California COUNTRY: United
                                                                                                                                                                                                                                                      100.0%; Score 131; DB 4; 100.0%; Pred. No. 1.3e-14;
                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                   TYPE: amino acid
STRANDEDNESS: <Unknown>
TYPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 112:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 113, Application US/08912951
Patent No. 6475789
GENERAL INFORMATION
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
TELEPHONE: (415) 576-0200
                      (415) 576-0300
                                                                                  LENGTH: 24 amino acids
                      TELEFAX: (415) 576-03(
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
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Harley, Calvin
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Best Local Similarity 100.0
Matches 24; Conservative
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                                                                                                                                                                                                              US-09-430-323-112
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NOTHER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                      Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 131; DB 3; Best Local Similarity 100.0%; Pred. No. 1.3e-14; Matches 24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
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APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                      015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FFYVTETTFQKONRLFFYRKSVWSK 24
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Patent No. 6309867
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
           CLASSIFICATION: 536
ATTORNEY/ACENT INFORMATION:
NAME: APPIE, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01538
TELECOMMUNICATION INFORMATION:
TELECHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION
01-OCT-1996
                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-854-050-112
                                                                                                                                                                                                                                                      TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-430-323-112
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APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND STREED: TWO ENDRESSE: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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peptide from human TRT"
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 100.0%; Score 131; DB 3; Similarity 100.0%; Pred. No. 2.4e-14; 24; Conservative 0; Mismatches 0;
                    FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17618
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: APPLE Randolph Ted
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/SOCKET NUMBER: 36,42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 FFYVTETTFOKNRLFFYRKSVWSK 37
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US 08/912,951
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FILING DATE: 14-AUG-1997
LASSIFICATION: 436
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 72, Application US/08912951
Patent No. 6475789
GENERAL INFORMATION:
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MOLECULE TYPE: peptide
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LOCATION: 1..43
OTHER INFORMATION:
OTHER INFORMATION:
APPLICATION NUMBER:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-974-549A-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-912-951-72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 131; DB 4; Length 24; Best Local Similarity 100.0%; Pred. No. 1.3e-14; Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 72. Application US/08974549A
Fatent No. 6166178
GENERAL INFORMATION:
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC compatible
OPERATING SYSTEM: PC compatible
OPERATING SYSTEM: PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIPICATION: DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1997
FILING DATE: 18-APR-1997
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/951,312
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: US 08/911,312
FILING DATE: US 08/911,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: California
COUNTRY: USA
                                                                015389-002600US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FFYVTETTFOKNRLFFYRKSVWSK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FFYVTETTFOKNRLFFYRKSVWSK 24
                 RECISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 0153/
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
Randolph T
                                                                                                                                                                                                                                                  LENGTH: 24 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-912-951-113
                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-974-549A-72
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Gaps
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CTHER INFORMATION: /note= "motif T peptide from human TRT"
US-08-974-549A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 131; DB 3; Length 48; Best Local Similarity 100.0%; Pred. No. 2.7e-14; Matches 24; Conservative 0; Mismatches 0; Indels
                                 PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                        CONTRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFTCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1936
RIDNG APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
RIDNG APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
RIDNG APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION NUMBER: US 08/911,312
PRIOR APPLICATION NUMBER: US 08/911,312
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 11-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 01-OCT-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 11-OCT-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 FFYVTETTFQKNRLFFYRKSVWSK 37
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Patent No. 6475789
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-912-951-30
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Patent No. 616618
GENERAL INFORMATION:
APPLICANT: Lingner, Joachim
APPLICANT: Capman: Aren B.
APPLICANT: Chapman: Karen B.
APPLICANT: Andrews, William H.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Languan: Applicant: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES. 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "telomerase specific motif T
peptide from human TRT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 2.4e-14;
Matches 24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                          PELECATION 1915
PRICATION 1915
PRICATION NUMBER: US 08/844,419
FILING DATE: 18 APR-1997
CLASSIFICATION NUMBER: US 08/724,643
PRIOR APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION: A35
ATTORNEY/AGENT INFORMATION:
NAME: ASDIGNEY
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAMENT (415) 576-0300
TELEFAX: (415) 576-0300
TELEFAX: (415) 576-0300
TELEFAX: (415) 576-0300
TELECOMMUNICATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
                                                                            PRICE APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FFYVTETTFQKNRLFFYRKSVWSK 24
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: p. US-08-912-951-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Two Embarcac
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Peptide LOCATION: 1..43
                                 FILING DATE: 09
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: O6-MAY-1997
CLASSIFICATION NUMBER: US 08/846,017
PRIOR APPLICATION NUMBER: US 08/846,017
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 01-OCT-1996
CLASSIFICATION:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
ATTOREY/AGENT INFORMATION:
REGISTRENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0300
INFORMATION PON SEQ ID NO: 67:
SEGUENCE CHRARCTERISTICS:
I-PNGTHH: 129 amino acids
                                                                                                                                                                                        APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESSONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States of America
                       Sequence 67, Application US/08851843A Patent No. 603809 GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-851-843A-67
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              APPLICANT: Unapmen, Waren B.
APPLICANT: Unapmen, Carego B.
APPLICANT: Morin, Carego B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND TITLE OF INVENTION: THERAPEUTIC METHODS
TOTALE: 335
CORRESPONDENCESS: 335
CORRESPONDENCESS: 335
CORRESPONDENCESS: 335
CONNEY: California Townsend and Crew LLP
STREET: Two Embarcadeso Center, 8th Floor
CONPUTER RADABLE FORM:
MEDIUM TYPE: RIPLOF COMPATION COMPATION AND THE Release #1.0, Version #1.30
COMPUTER: Tabe Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 09-MY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 63-ARP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-ARP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 35-ARP-1997
FILING DATE: 35-ARP-1997
FILING DATE: 18-ARP-1997
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100.0%; Score 131; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.7e-14;
Matches 24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                015389-002600US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FFYVTETTFOKNRLFFYRKSVWSK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randalph T.
REGISTRATION NUMBER: 16,429
REFERENCE/DOCKET NUMBER: 01538
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 amino acids
TYBE: amino acids
  Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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Gaps
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                                                                                                                                       NAME/KEY: Peptide

LOCATION: 1..129

COTHER INFORMATION: /note= "TRT motifs from human"

US-08-851-843A-67
                                                                                                                                                                                                                                                                                                                                                       1 FFYVTETTFOKNRLFFYRKSVWSK 24
                                                                                                                                                                                                                                                                                                                                                                                               19 FFYVTETTFOKNRLFFYRKSVWSK 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-08-974-549A-13
; Sequence 13, Application US/08974549A
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS:
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14 FFYVTETTFQKNRLFFYRKSVWSK 37

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TELEPHONE: (415) 576-0200 TELEPAX: (415) 576-0300 INFORMATION FOR SEC ID NO: 67; SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                          8
               APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INTENTION: Human Telomerase Catalytic Subunit
                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INPORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEC ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 129 amino acide
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Peptide
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Patent No. 6166178
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USCAPION: 1.1199

UGORITON: 1.1199

USCAPITATION: 1.1199

USCAPITATION: 1100.04; SCOTE 111; DB 3; Length 129; Best Local Smilarity 100.04; SCOTE 111; DB 3; Length 129; Best Local Smilarity 100.04; SCOTE 111; DB 3; Length 129; Best Local Smilarity 100.04; Pred. No. 78e-14.

OV 1817 SMILARITY 100.04; Pred. No. 78e-14.

DD 19 FFYVIETTORNILPYRKSWSK 42

RESULT 12

USCAPE 100.04

SEQUENCE 67, APPLICATION USCAPE 100.04

SEQUENCE 67, APPLICATION USCAPE 100.04

SEQUENCE 67, APPLICATION USCAPE 100.04

APPLICANT: Cally INTENDED 100.04

STREET: Two Embarcadero Center, 8th Floor

CONRESCENT: Two Embarcadero Center, 8th Floor

STREET: Two Embarcadero Center, 8th Floor

CONRESCENT: Cally INTENDED 100.04

APPLICANT: United States of America

CONRESCENT: Two Embarcadero Center, 8th Floor

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STREET: Two Embarcadero Center, 8th Floor

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STREET: APPRICATION NOTES:

CONNERS: Callifornia

STREET: Two Embarcadero Center, 8th Floor

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STREET: Two Embarcadero Center, 8th Floor

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STREET: Two Embarcadero Center, 8th Floor

STREET: Two Embarcadero Center, 8th Floor

STREET: APPRICATION NOTES:

APPLICATION NOMES: US 08/846,017

FILING DATE: 10-APR.1997

FILING DATE:
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APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
TITLE OF INVENTION: THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                         Gaps
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                                                                                              Length 129;
OTHER INFORMATION: /note= "TRT motifs from human" SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE STATEMENT OF THE SECONDARY SOFTWARE STATEMENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION NUMBER: US 08/854,050
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FLING DATE: 09-MAY-1997
CLASSIFICATION ATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                            100.0%; Score 131; DB 4;
100.0%; Pred. No. 7.8e-14;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              015389-002600US
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APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                   1 FFYVTETTFOKNRLFFYRKSVWSK 24
                                                                                                                                                                                                                                19 FFYVTETTFOKNRLFFYRKSVWSK 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/08912951; Patent No. 6475789; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36,429
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,4
                                                                              Query Match
Best Local Similarity 100.0
Warches 24; Conservative
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CLASSIFICATION: 435
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APPLICANT:
APPLICANT:
                                 ,
US-09-430-323-67
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APPLICANT:
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                                                                                                                                         Length 129;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: «Unknown.»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION DAMER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APP-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
APPLICATION NUMBER: US 08/724,643
APPLICATION NUMBER: US 08/724,643
ATTORNEY/AGENT INPORMATION:
NAME: Apple: Raddiph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELLCOMMUNICATION:
                                                                       /note= "TRT motifs from human"
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 67, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
CECH, Thomas R.
Lingner, Joachim
NAkamura, Toru
Chapman, Karen B.
Morin, Greeg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend and Crew
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                  ch 100.0%; Score 131; DB 3;
1 Similarity 100.0%; Pred. No. 7.8e-14;
24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States of America
                                                                                                                                                                                                                                                        19 FFYVTETTFQKNRLFFYRKSVWSK 42
                                                                                                                                                                                                                                1 FFYVTETTFOKNRLFFYRKSVWSK 24
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SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
1..129
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                          ; NAME/KEY: Peptide
; LOCATION: 1..129
; OTHER INFORMATION:
US-08-854-050-67
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LOCATION:
                                                                                                                                                            Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-09-430-323-67
                                                                                                                                           Query Match
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NAME/KEY: Protein
LOCATION: 1..259
OTHER INFORMATION: /note= "protein encoded by clone 712562"
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            PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-0CT-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-0CT-1997
ATTORNEY/ACENT INFORMATION:
NAME: APPLICATION NUMBER: 36,429
REGISTATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: November 12, 2003, 19:53:26 Job time : 11.1698 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 FFYVTETTFQKNRLFFYRKSVWSK 35
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14-AUG-1997
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Best Local Similarity 100.
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/08974549A
; Sequence 10, Application US/08974549A
; GENERAL INFORMATION:
    APPLICANT: Cech, Thomas R.
    APPLICANT: Lingner, Joachim
    APPLICANT: Informar, Toru
    APPLICANT: Namura, Toru
    APPLICANT: Morin, Gaegg B.
    APPLICANT: Andrews, William H.
    TITLE OF INVENTION: Human Telomerase Catalytic Subunit
    TITLE OF INVENTION: Human Telomerase Catalytic Subunit
    NUMBER OF SEQUENCES: 727
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew LLP
    STREET: Two Embarcadero Center, Eighth Floor
    CITY: San Francisco
    STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 10-OCT-1996
RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
RRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 08-MAY-1997
RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
RRIOR APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
RRIOR APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
RRIOR APPLICATION NUMBER: US 08/915,503
                                                                                                                                           NAME/KEY: Peptide

LOGATION: 1..129

CTHER INFORMATION: /note= "TRT motifs from human"

US-08-912-951.
                                                                                                                                                                                                                                                                                                                                                                                                 1 FFYVTETTFOKNRLFFYRKSVWSK 24
LENGTH: 129 amino acids
TYPE: amino acid
                    TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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Sequence:

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Patent No. US2002016478641

GENERAL INFORMATION:
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
TITLE OF INVENTION: No. US20020164786A1e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCES: 225
CORPUTER: United States of America
COUNTRY: United States of America
SIP: 94411
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: DEALERIEN RELABBRE FORM:
COMPUTER: DEALERIEN RELABBRE PROPERIENT PAPE: PLOUP NATA.
            US-10-054-295-67

US-10-044-519-13

US-10-044-539-13

US-10-044-539-10

US-10-044-539-10

US-10-044-539-10

US-10-282-960-3

US-10-282-960-3

US-10-282-960-81

US-10-282-960-81

US-10-282-960-81

US-10-282-960-81

US-10-282-960-81

US-10-282-101

US-10-054-295-101

US-10-064-539-55-50

US-10-064-539-55-50
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US-09-749-728B-31
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US-09-953-052-2
US-10-295-681-57
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APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/854,050
APPLICATION NUMBER: US/08/854,050
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US/08/846,017
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1997
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1003
                                                                      100.0
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(without alignments)
215.025 Million cell updates/sec
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                                                                                                                               November 12, 2003, 19:47:20 ; Search time 19.1698 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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Sequence
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                GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-843-676-112
US-09-766-253-112
US-00-053-758-112
US-10-054-295-112
US-10-054-295-112
US-10-044-692-113
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US-10-044-692-72
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US-10-044-539-30
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US-10-94-818-67-67
US-09-438-486-67
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Maximum Match 100%
Listing first 45 summaries
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                                                                                            - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                              US-08-854-050-112
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Match Length
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Gaps
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0
                                                                                                                                         Length 24;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486 FILING DATE: 12-NOV-1999 CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                    Ouery Match 100.0%; Score 131; DB 10; Best Local Similarity 100.0%; Pred. No. 2.1e-13; Matches 24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
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NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                      TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-09-766-253-112
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FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States of America ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                    1 FFYVTETTFOKNRLFFYRKSVWSK 24
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FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 112, Application US/09438486; Publication No. US20030009019A1; GENERAL INFORMATION:
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
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STRANDEDNESS:
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100.0%; Score 131; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.1e-13;
Matches 24; Conservative 0; Mismatches 0; Indels
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MEDLUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/766,253

FILING DATE: 19-Jan-2001

CLASSIFICATION: CUNKNOWN>

PRIOR APPLICATION: CUNKNOWN>

FILING DATE: 1997-04-25

APPLICATION NUMBER: US 08/846,017

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020187471Alel Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, 8th Floor
              ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: California COUNTRY: United States of America
                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-09-843-676-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 112, Application US/09766253
Publication No. US20020187471A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Inigner, Joachim
Nakamura, Toru
Nakamura, Toru
Mayamira, Karen B.
Morin, Gregg B.
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FILING DATE: 01-OCT-1996
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LENGTH: 24 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California COUNTRY: United States of America ZIP: 94111 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: ISAN PC Compatible OPERATICS YSTEM: PC-COMPUTER: PATENTIC SYSTEM: PC-COMPUTER: PATENTIC RELEASE #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                  Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO US20030044953Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
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  Indels
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 131; DB 15;
100.0%; Pred. No. 2.1e-13;
ive 0; Mismatches 0;
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APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-04n-2002
CLASSIFICATION: 316
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050
FILING DATE: CUNKNOWN:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
  Mismatches
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 112:
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                                                1 FFYVTETTFQKNRLFFYRKSVWSK 24
                                                                                         1 FFYVTETTFOKNRLFFYRKSVWSK 24
                                                                                                                                                                                                         Sequence 112, Application US/10054295
Publication No. USZ0030044953A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FELEPHONE: (415) 576-0200
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24; Conservative
  24; Conservative
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Best Local S
Matches 24
  Matches
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                                                                                            Length 24;
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Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030032075Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 131; DB 15;
Pred. No. 2.1e-13;
                                                                                       Query Match
100.0%; Score 131; DB 11;
Best Local Similarity 100.0%; Pred. No. 2.1e-13;
Matches 24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
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COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/10/053,758 FILING DATE: 18-Jan-2002 CLASSIFICATION: 536
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SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-053-758-112
                                                                                                                                                                                     1 FFYVTETTFOKNRLFFYRKSVWSK 24
                                                                                                                                                                                                                                   1 FFYVTETTFOKNRLFFYRKSVWSK 24
                                                                                                                                                                                                                                                                                                                                                 Sequence 112, Application US/10053758
Publication No. US20030032075A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (415) 576-0200
15) 576-0300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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                        MOLECULE TYPE: peptide
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111
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Best Local Similarity
                                           US-09-438-486-112
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TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/10/044,692

FILING DATE: 11-Jan-2002

CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                      NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Twomsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,425
REFERENCE/DOCKET NUMBER: 015389-002600US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 131; DB 15; Best Local Similarity 100.0%; Pred. No. 2.1e-13; Matches 24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/912,951
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 10-OCT-1996
                                                                                                                                                                                                                                STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 113:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 113, Application US/10044539 Publication No. US20030100093A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Morin, Gregg B.
Harley, Calvin
Andrews, William H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 5
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-044-539-113
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                                                                                  APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030059787A1e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STRATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94111

COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: 1BM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/10/054,611
    FILING DATE: 18-Jan-2002
    CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 131; DB 15;
100.0%; Pred. No. 2.1e-13;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/854,050
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-054-611-112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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Publication No. USZ0030096344A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                      Sequence 112, Application US/10054611
Publication No. US20030059787A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-044-692-113
US-10-054-611-112
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Morin, Gregg B.
Haritey, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
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                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NAMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <UNknown>
                        ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 131; DB 15; 100.0%; Pred. No. 3.9e-13;
                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: «UNKNOWN»
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
                                                                                        STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide from human TRT"
SEQUENCE DESCRIPTION: SEQ ID NO: 72:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 72, Application US/10044539
Publication No. US20030100093A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chapman, Karen B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
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Best Local
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TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIAGNOSTIC AND
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TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT:
THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 24;
                                                                                                                                                                                                                                                  COMPUTER: FLORDY disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION BATE: US/10/044,539
FILING DATE: 1-Jan-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATE: 08/912,951
FILING DATE: <UNKNOWN:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 05-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                          NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 100.0%; Score 131; DB 15; 1 Similarity 100.0%; Pred. No. 2.1e-13; 24; Conservative 0; Mismatches 0;
                                                                                                                                                              STATE: California
COUNTRY: United States of America
ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-044-539-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FFYVTETTFOKNRLFFYRKSVWSK 24
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GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Greeg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (415) 576-0200
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Publication No. US20030096344A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 113:
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                                                                                                                                            CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (415)
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Best Local Similarity
Matches 24; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-10-044-692-72
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HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: /note= "motif T peptide from human TRT SEQUENCE DESCRIPTION: SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ENDOPED STATES OF THE STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Twomsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 131; DB 15; Best Local Similarity 100.0%; Pred. No. 4.4e-13; Matches 24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: «UNREDENT D8/464,050
APPLICATION NUMBER: US 08/854,050
APPLICATION NUMBER: US 08/81,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/74,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                        STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FFYVTETTFOKNRLFFYRKSVWSK 24
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Andrews, William H. TITLE OF INVENTION: HUMAN TELC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 30, Application US/10044539
Publication No. US20030100093A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: <Unknown>TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 48 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Morin, Gregg B.
                                                                                                   SEQUENCES: 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-044-539-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 43;
                                                                                                                                                                                                                  COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,539
FILING DATE: 11.-Jan-2002
CLASSIFCATION BATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                               NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 131; DB 15;
100.0%; Pred. No. 3.9e-13;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/912,951
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
ATTONNEY/AGENT INFORMATION:
   THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide from human TRT"
SEQUENCE DESCRIPTION: SEQ ID NO: 72:
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Publication No. US20030096344A1
GENERAL INFORMATION:
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 576-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 43 amino acids
                                                                                                                                                              CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1..43
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 576-(
INFORMATION FOR SEQ ID NO: 72
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.1
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-10-044-692-30
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Gaps
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SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-843-676-67
                                                                                                                                                                                                                          COUNTEY: United States of America

ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
RELING DATE: 26-Apr-2001
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Hariley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020187471A1el Telomerase
              Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. US20020164786A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/654,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REFERENCE/DOCKET NUMBER: 36,429
TELECOMMUNICATION INFORMATION:
                                                                                                                   STREET: Two Embarcadero Center, 8th Floor
STREE: San Francisco
STATE: Calif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 131; DB 10; Best Local Similarity 100.0%; Pred. No. 1.2e-12; Matches 24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 FFYVTETTFQKNRLFFYRKSVWSK 42
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TELEFAX: (415) 576-0300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 67
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                      Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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OTHER INFORMATION: /note= "motif T peptide from human TRT"
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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                                                                                                       CORRESPONDED ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
STATE: California
CONTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REPERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 131; DB 15;
100.0%; Pred. No. 4.4e-13;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: «Unknown»
APPLICATION NUMBER: 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 FFYVTETTFQKNRLFFYRKSVWSK 37
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Patent No. US20020164786A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Tocuu
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 48 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
Harley, Calvin
                                                                                          NUMBER OF SEQUENCES: 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.'
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 25-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/44,419
FILING DATE: 10-CCT-1996
CLASSIFICATION NUMBER: 36,429
FILING DATE: 10-CCT-1996
CLASSIFICATION NUMBER: 36,429
FILING DATE: 01-CCT-1996
CLASSIFICATION DATE: 01-CCT-1996
CLASSIFICATION NUMBER: 01-CCT-1996
CLASSIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1.129
OTHER INFORMATION: /note= "TRT motifs from human"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 131; DB 11; 100.0%; Pred. No. 1.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: November 12, 2003, 19:55:46
Job time : 19:1698 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 FFYVTETTFORNRLFFYRKSVWSK 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 100.(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-438-486-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 131; DB 10; Length 129; Best Local Similarity 100.0%; Pred. No. 1.2e-12; Matches 24; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1.129
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                          CORPUTER: FORPY disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 67, Application US/09438486
Publication No. US2003009019A1
GENERAL INFORMATION
APPLICANT: Cach, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Morin, Greeg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US20030009019A1e1 Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFRENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FFYVTETTFQKNRLFFYRKSVWSK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : California
RY: United States of America
94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acids
STRANDEDNESS: «Unknown»
                              NUMBER OF SEQUENCES: 171
                                                                                                                                                                                                                                                 ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
STATE: California
COUNTRY: United Stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-09-438-486-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
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Gaps

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Length 129; Indels

THIS PACK BLANK TON TO

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

November 12, 2003, 19:43:04 ; Search time 9.35849 Seconds (without alignments) 246.626 Million cell updates/sec Run on:

US-08-854-050-112

131 1 FFYVTETTFQKNRLFFYRKSVWSK 24 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 Total number of hits satisfying chosen parameters:

283308 segs, 96168682 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

pir 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | telomerase catalyt | telomerase catalyt | telomerase reverse | telomerase (EC 2.7 | hypothetical prote | telomerase reverse | hypothetical prote | prl1/prl2-like pro | hypothetical prote | | hypothetical prote | _ | hypothetical prote | probable carbamoyl | probable carbamoyl | bo-type ubiquinol | cytochrome O ubiqu | hypothetical prote | actin depolymerizi | conserved hypothet | probable inner mem | probable transport | hypothetical prote | protein F12K21.20 | bo-type ubiguinol | cytochrome o ubiqu | bo-type ubiquinol | cytochrome o ubiqu | rd. |
|-----------|-----------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|-------------------|--------------------|--------|
| SUMMARIES | ID | T03844 | T03838 | T31107 | T14891 | B84462 | T51517 | T51884 | B90114 | AI2560 | A46616 | AH2143 | E86833 | F65070 | G91096 | C85942 | H84984 | AE0384 | T50155 | G84717 | G71276 | A47649 | E95982 | T05510 | H86468 | A85540 | E90689 | B42226 | 0 | T38804 |
| | DB | 7 | 7 | 7 | 7 | ~ | 64 | ~ | ~ | Ŋ | ~ | N | ~ | ~ | ~ | ~ | 7 | N | ~ | ~ | 7 | ~ | ~ | N | 7 | 7 | ~ | ~ | ~ | 7 |
| عن | Query Match Length | 1132 | 989 | 1132 | 1117 | 389 | 1123 | 205 | 306 | 345 | 791 | 270 | 277 | 363 | 396 | 396 | 662 | 663 | 762 | 132 | 294 | 420 | 420 | 545 | 602 | 663 | 663 | 663 | 663 | 695 |
| | Query | 100 | 53.4 | $^{\circ}$ | œ | 2 | 39.7 | ۲. | 36.6 | 36.3 | 35.9 | 35.1 | 35.1 | 35.1 | 35.1 | 35.1 | 35.1 | 35.1 | 35.1 | 34.7 | 34.7 | 34.4 | 34.4 | | 34.4 | 34.4 | 4 | 34.4 | 4 | 34.4 |
| | Score | 131 | 70 | 69 | 63 | 55 | 52 | 49 | 48 | 47.5 | 47 | 46 | 46 | 46 | 46 | 46 | 46 | 46 | 46 | • | • | 45 | 45 | 45 | 45 | 45 | 45 | 45 | 45 | 45 |
| | Result No. | - | 61 | e | 4 | S | 9 | 7 | 89 | σ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | | | 21 | | | 24 | 25 | 26 | 27 | 28 | 29 |

| ct234 hypothetical | conserved hypothet | CT234 hypothetical | dynein heavy chain | hypothetical prote | | hypothetical prote | hypothetical prote | conserved hypothet | hypothetical prote | hypothetical 47.4 | capsular polysacch | NADH2 dehydrogenas | hypothetical prote | hypothetical prote | calcium-activated |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|-------------------|
| A72096 | E81573 | E86527 | T43274 | 139826 | C83911 | T41951 | T22536 | F70158 | T26918 | E65146 | T44650 | T12123 | T33028 | AE1590 | T46609 |
| ~ | ~ | 7 | 7 | 7 | 7 | 7 | ~ | ~ | ~ | 7 | ~ | ~ | ~ | ~ | ~ |
| 925 | 925 | 925 | 4196 | 385 | 184 | 239 | 263 | 273 | 351 | 412 | 466 | 683 | 712 | 445 | 1237 |
| | | 4. | 4.4 | 4.0 | 33.6 | 33.6 | 33.6 | 33.6 | 33.6 | 33.6 | 33.6 | 33.6 | 33.6 | 33.2 | 33.2 |
| 34.4 | 34.4 | 34 | ň | | | | | | | | | | | | |
| 45 34.4 | 45 34.4 | 45 34 | 45 3, | | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 43.5 | 43.5 |

ALIGNMENTS

```
telomerase catalytic chain - human
N;Alternate names: telomerase reverse transcriptase
C;Species: Homo sapiens (man)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C;Accession: T03844
R;Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J. Science 277, 955-959, 1997
A;Title: Telomerase catalytic subunit homologs from fission yeast and human.
A;Reference number: Z15111; MUID:97400623; PMID:9252327
A;Accession: T03844
A;Accession: T03844
A;Accession: T03844
A;Residues: 1-132 kMAk>
A;Residues: 1-132 kMAk>
A;Cross-references: EMBL:AF015950; NID:92330016; PIDN:AAC51672.1; PID:92330017
A;Experimental source: kidney
C;Genetics:
A;Acmeric TRT
RESULT 1
T03844
```

A; Map position: 5p

Gaps .. O ch 100.0%; Score 131; DB 2; Length 1132; 1 Similarity 100.0%; Pred. No. 3.4e-12; 24; Conservative 0; Mismatches 0; Indels 0; Query Match Best Local S Matches 24

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560 FFYVTETTFQKNRLFFYRKSVWSK 583 1 FFYVTETTFOKNRLFFYRKSVWSK 24 ò d

Toggasa telomerase catalytic chain - fission yeast (Schizosaccharomyces pombe)
NyAlternate names: telomerase reverse transcriptase 1
C;Species: Schizosaccharomyces pombe
C;Date: 23-Apr-1999 #sequence revision 23-Apr-1999 #text_change 01-Dec-2000
C;Accession: T03818; T03839; T40085
R;Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J Science 277, 955-959, 1997
A;Title: Telomerase catalytic subunit homologs from fission yeast and human.
A;Reference number: Z15111; MUID:97400623; PMID:9252327
A;Accession: T03818
A;Accession: T03818
A;Retius: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-999 *NAK>
A;Cross-references: EMBL:AF015783; NID:92340167; PIDN:AAC49803.1; PID:92340169
A;Experimental source: strain 972h(-)
A;Accession: T03839
A;Cross-references: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-524,526-989 *NAZ>
A;Residues: 1-524,526-989 *NAZ>
A;Residues: 1-524,526-989 *NAZ>
A;Residues: 1-524,526-989 *NAZ>
A;Cross-references: EMBL:AF015783; NID:92340167; PIDN:AAC49802.1; PID:92340168

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```
hypothetical protein At2g04840 [imported] - Arabidopsis thaliana (C.Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: Dateb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 (C.Specession: B84462 (C.Speciession: B84462 (C.Spec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 5
A;Introns: 100/3; 125/3; 147/3; 185/1; 300/3; 325/1; 369/2; 414/3; 765/3; 942/2; 1033/2
A;Note: F5E19_190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   telomerase reverse transcriptase - Arabidopsis thaliana
N'Alternate names: protein F5E19 190
S'Species: Arabidopsis thaliana (Mouse-ear cress)
C'Species: Arabidopsis thaliana (Mouse-ear cress)
C'Species: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C'Accession: T51517
R'Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, submitted to the Protein Sequence Database, August 2000
A'Reference number: 225394
A'Accession: T51517
A'Accessio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE002093; NID:g4544413; PIDN:AAD22322.1; GSPDB:GN00139 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
TS1884
TS1884
TS1884
(hypothetical protein DKFZp547K054.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.0%; Score 55; DB 2; Length 389; 47.6%; Pred. No. 0.82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                               Indels
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Pred. No. 7.1;
                  0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                          7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Mismatches
                  42.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | | | | : :::|| | : 559 FYATESQGGRLNIYYYRKRSWER 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 FYVTETTFOKNRLFFYRKSVWSK 24
                                                                                                                                                                                                 476 FYITEKHKEGSQIFYYRKPIW 496
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                                                                                                                                                2 FYVTETTFQKNRLFFYRKSVW
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34.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 47.6
Matches 10; Conservative
                                                      9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Best Local Similarity
         Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: At2g04840
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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NyAlternate names: telomerase reverse transcriptase
CiSpecises: Tetrahymena thermophila
CiSpecises: Tetrahymena thermophila
CiSpecises: Tetrahymena thermophila
CiAccession: T14891
RiCollins, K.; Gandhi, L.
RiCollins, K.; Gandhi, L.
RiCollins, K.; Gandhi, L.
RiCollins, K.; Gandhi, L.
RiCollins, R.; Gandhi, L.
A; Reference number: Z18252; MUID:98337941; PMID:9671704
A; Reference number: Z18252; MUID:98337941; PMID:9671704
A; Reference number: Z18252; MUID:98337941; PMID:9671704
A; Residues: 1117 cCOL>
A; Residues: 1-1117 cCOL>
A; Cross-references: EMBL:AF061284; NID:g3335166; PID:g3335167; PIDN:AAC39140.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      telomerase reverse transciptase - Oxytricha trifallax
C;Species: Oxytricha trifallax
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C;Accession: T31107
R;Bryan, T.M.; Sperger, J.M.; Chapman, K.B.; Cech, T.R.
Proc. Natl. Acad. Sci. U.S.A. 95, 8479-8484, 1998
A;Title: Telomerase reverse transcriptase genes in Tetrahymena thermophila and Oxytricha A;Reference number: Z20985; MUID:98337940; PMID:9671703
A;Accession: T31107
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 2
A;Introns: 86/3; 113/3; 153/2; 241/1; 372/1; 395/3; 485/3; 524/3; 582/2; 644/1; 693/3;
C;Keywords: alternative splicing
                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-524,226-989 <LYN>
A;Residues: 1-524,226-989 <LYN>
A;Cross-references: EMBL:AL022299; PIDN:CAA18391.1; GSPDB:GN00067; SPDB:SPBC29A3.14c
A;Experimental source: strain 972h-; cosmid c29A3
C;Genetics:
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A;Cross-references: EMBL:AF060230; NID:g3342795; PID:g3342796; PIDN:AAC39163.1
C;Genetics:
A;Gene: TERT
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Pred. No. 0.016;
7; Mismatches 6; Indels
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R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G. submitted to the EMBL Data Library, March 1998
A;Reference number: Z21904
A;Accession: T40085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 53.4%; Score 70; DB 2; Le Best Local Similarity 45.5%; Pred. No. 0.0097; Matches 10; Conservative 7; Mismatches 5;
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A,Genetic code: SGC5
C,Keywords: nucleotidyltransferase
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1 Similarity 43.5%;
10; Conservative
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Matches 10; Conserv
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A46616

A46616

Cytochrome—c oxidase (EC 1.9.3.1) chain I - Thermus aquaticus

Cytochrome—c oxidase (EC 1.9.3.1) chain I - Thermus aquaticus

Cytochrome claa3 55K chain; cytochrome claa3 large chain

C;Species: Thermus aquaticus

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 11-May-2000

C;Accession: A46616; S03949

R;Mather, M.W.; Springer, P.; Hensel, S.; Buse, G.; Fee, J.A.

J. Biol. Chem. 268, 5395-5408, 1993

A;Title: Cytochrome oxidase genes from Thermus thermophilus. Nucleotide sequence of the A;Reference number: A46616; MUID:93194828; PMID:8383670

A;Accession: A46616

A;Accession: A46616

A;Accession: A46616

A;Accession: Breiminary

A;Residues: 1-791 cMAT>

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A;Residues: 1-791 cM
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A; Rote: the source is designated as Thermus thermophilus

R; Buse, G.; Soulimane, T.; Dewor, M.; Meyer, H.E.; Blueggel, M.

Protein Sci. 8, 985-990, 1999

Protein Sci. 8, 985-990, 1999

P; Reference number: A58960; MUID: 99268331; PMID: 10338009

A; Reference number: A58960; MUID: 99268331; PMID: 10338009

A; Contents: annotation

A; Note: mass spectrographic and chemical characterization of histidyl-tyrosine cross-link

C; Superfamily: cytochrome-c oxidase chain I/III; cytochrome-c oxidase chain I homology

C; Keywords: chromoprotein; copper; electron transfer; heme: iron; magnesium; membrane-a F; 23-469; Domain: cytochrome-c oxidase chain I homology Col)

F; 23-469; Domain: cytochrome-c oxidase chain I homology Col)

F; 23-46; Domain: cytochrome-c oxidase chain I homology Col)

F; 250, 299; 300/Binding site: heme a iron (His) (axial ligands) #status predicted

F; 254, Binding site: magnesium (His) (axial ligand) #status predicted

F; 3377/Binding site: magnesium (His) (axial ligand) #status predicted

F; 3377/Binding site: heme a iron (His) (axial ligand) #status predicted
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AH2143

AH2143

Protein all2703 [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C;Accession: AH2143

R;KaneKo, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                   Gaps
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        DB 2;
    Query Match
36.3%; Score 47.5; E
Best Local Similarity 50.0%; Pred. No. 11;
Matches 11; Conservative 2; Mismatches
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A.Title: The highly reduced genome of an enslaved algal nucleus.
A.Accession: B90114
A.Status: preliminary
A.Notecule type: DNA
A.Notecule type: DNA
A.Rotessidus: 1-306 - DOU>
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:2159285; PMID:11759840
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A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C,Accession: A12560
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A,Readduds: 1-345 <KUR>
A,Readduds: 1-345 <KUR>
A;Cross-references: Bs.AP003603; PIDN:BAB77410.1; PID:g17134853; GSPDB:GN00182
A,Experimental source: strain PCC 7120
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R;Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Weil, B.; Wiemann, submitted to the Protein Sequence Database, July 2000
A;Reference number: 225853
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Pred. No. 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Indels
                                                                                                                      A;Accession: T51884
A;Status: preliminary
A;Molecule type: mRAA
A;Residues: 1-205 «AAA>
A;Cross-references: EMBL;AL390175
A;Cross-references: fetal brain; clone DKFZp547K054
A;Note: DKFZp547K054.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 49; DB ?
Pred. No. 3.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 ISETTEGSNALYHVHQIVWGR 173
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61.5%;
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202 TSISKNEIFFYRK 214
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Matches 8; Conservative
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A;Genome: nucleomorph
C;Keywords: nucleomorph
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probable carbamoyl transferase [imported] - Escherichia coli (strain O157:H7, substrain Cispecies: Escherichia coli Cispecies: Escherichia coli Cispecies: Bedul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 Cispecies: Both Cispecies: Cis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable carbamoyl transferase Z4209 [imported] - Escherichia coli (strain O157:H7, sub C;Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: C859-2001 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Accession: C85942 A;Accession: C85942 A;Accession: C85942 A;Status: preliminary A;Nolecule type: DNA A;Residues: 1-396 <CEO.
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A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: GB:BA000007; PIDN:BAB37166.1; PID:g13363215; GSPDB:GN00154
A,Experimental source: strain O157:H7, substrain RIMD 0509952
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Pred. No. 21;
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5; Mismatches
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345 VTEGVFEKYRIATYKEASW 363
   321 VTEGVFEKYRIATYKEASW 339
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42.1%;
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42.1%;
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Best Local Similarity
Matches 8; Conserve
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Best Local Similarity
Matches 8; Conserv
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C;Date: 23.Mar-2001 #sequence_revision 23.Mar-2001 #text_change 03.Aug-2001
C;Accession: B86831
R;Bolotin, A; Mincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se A;Reference number: A86625; MUD:21235186; PMID:11337471
A;Accession: B86833
A;Status: preliminary
A;Molecule type: DNA
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C.Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C.Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C.Bactesion: F65070
R.Bactener, F.R:; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A.Title: The complete genome sequence of Escherichia coli K-12.
A.Reference number: A64720; MUID:97426617; PMID:9278503
A.Accession: F65070
A.Accession: F65070
A.Accession: F65070
A.Residues: 1-363 <BLAT>
A.Cross-references: GB.AE000370; GB.U00096; NID:92367170; PIDN:AAC75908.1; PID:g1789234; A.Seperimental source: strain K-12, substrain MG1655
C.Superimental source: strain K-12, substransferase homology
F;1-352/Domain: aspartate/ornithine carbamoyltransferase homology ACT>
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                           A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-270 «KUR»
A;Cross-references: GB:BA000019; PIDN:BAB74402.1; PID:g17131796; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics: A;Gene: a112703
C;Superfamily: Synechocystis hypothetical protein sll1774
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Pred. No. 19;
5; Mismatches 6; Indels
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Pred. No. 15;
6; Mismatches
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Pred. No.
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47.1%;
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Best Local Similarity 42.1%;
Matches 8; Conservative
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Best Local Similarity 30.4%;
Matches 7; Conservative
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Best Local Similarity 47.11
Best Local 8; Conservative
A; Accession: AH2143
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